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| (54) Title: PLANT GENETIC TRANSFORMATION METHODS AND TRANSGENIC PLANTS (57) Abstract An efficient transformation system for plants has been developed that yields high transformation efficiencies and pure transgenic plants and products thereof. Genomic integration of transgenes was confirmed by genomic DNA hybridization analysis. Pure transgenic plants have been successfully established in soil. Pure transgenic products of these plants have been produced. | | |

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PLANT GENETIC TRANSFORMATION METHODS AND TRANSGENIC PLANTS

FIELD OF THE INVENTION

- 5 The present invention relates to genetic transformation methods useful for the stable introduction of DNA sequences into the genomes of plants. Further the invention includes transgenic raspberry and strawberry plants.

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BACKGROUND OF THE INVENTION

Red raspberries (*Rubus idaeus* L.) have become important temperate fruit crops.

10 "Meeker", "Chilliwack" and "Canby" are major cultivars grown in the Pacific North West (PNW) of America -- one of the major producers of red raspberry in the world. Cultivar Meeker is the most widely planted raspberry cultivar in the PNW because of its high yield and resistance to diseases (Moore and Daubeney, 1993).

The potential for cultivar improvement through traditional breeding methods is

15 limited in *Rubus* due to the heterozygous nature of the species and its severe inbreeding depression. It can take 20 to 30 years to breed a *Rubus* cultivar with a characteristic transferred from unimproved germ plasm (Jennings and McNicol, 1991).

Strawberries (*Fragaria X ananassa*) are an important fruit crop with worldwide production of about 2.4 million tons annually. The perishable nature of the crop contributes

20 to significant losses to the fresh market industry (Ceponis and Butterfield, 1973; Kader, 1991; Wright and Billeter, 1975). The principal cause of post harvest losses in strawberry is gray mold (*Botrytis cinerea*), most often associated with softening, bruising and leaking of the fruit (El-Kazzaz, M.K., *et al.*, 1983). The narrow genetic base of the cultivated strawberry (Sjulin and Dale, 1987) and its polyploid nature and heterozygosity limit the

25 potential for improvement by traditional breeding methods.

Gene transfer technology allows introduction of new traits in proven cultivars without disrupting their otherwise desirable genetic constitutions. However, the recalcitrant nature and poor transformation rate of woody species have placed them far behind the herbaceous group in the application of gene transfer methods (Schuerman and Dandekar,

30 1993).

The work described herein, discloses the incorporation of heterologous genes into red raspberries, specifically, the first time generation of transgenic red raspberry cultivars Meeker, Chilliwack, and Canby. Also disclosed is the generation of transgenic strawberry cultivars Tristar and Totem.

SUMMARY OF THE INVENTION

The present invention includes a method for producing transgenic plants. In the method of the present invention, an expression vector having at least a first DNA sequence that encodes a gene encoding a selectable marker functional in plant cells is introduced into
5 cells of a target explant. This first DNA sequence is flanked by regulatory elements effective to allow expression of the sequence in plant host cells. Further, expression of this selectable marker gene produces a gene product that confers the ability of plant cells expressing the gene to grow in the presence of a selective agent. Exemplary selective agents include hygromycin, geneticin (G418) and kanamycin. Exemplary selectable marker
10 genes include *NPTII* and *hpt*.

In one embodiment, the expression vector is an *Agrobacterium*-type vector.

The expression vector is introduced into cells of a target plant tissue explant under conditions to generate transformation of explant cells. In one embodiment, the vector is introduced by co-culturing a target explant in the presence of *Agrobacterium* containing the
15 vector under conditions to generate transformation of explant cells by the vector. Typically, the co-culturing is carried out in liquid for from about 1 to about 3 days. Introduction of the vector into plant cells can also be carried out by other means, including, but not limited to, the following direct transformation methods: electroporation, microinjection, and microprojectile bombardment.

20 The plant tissue explant can be obtained from a variety of plant tissues including, but not limited to, leaf, petiole and meristem.

Transformed explant cells are then screened for their ability to be cultured in selective media having a threshold concentration of selective agent. Explants that can grow on the selective media are typically transferred to a fresh supply of the same media and
25 cultured again. The explants are then cultured under regeneration conditions to produce regenerated plant shoots. These regenerated shoots are used to generate explants. These explants from selected, regenerated plant shoots are then cultured on a higher concentration of selective agent. This iterative culture method is repeated until pure transgenic explants are obtained. The present invention also includes pure transgenic explants.

30 In one embodiment, pure transgenic explants are identified by dividing the regenerated plant shoots into explants, culturing the explants, and verifying that the growth of all explants is resistant to the highest concentration of selective agent used. That is, in the presence of selective agent there is no necrosis or significant bleaching of the explant tissue.

When pure transgenic explants are verified, transgenic plants are produced by regenerating plants from the pure transgenic explants. The present invention also includes pure transgenic regenerated plant shoots.

The vectors used in the method of the present invention may also include further
5 DNA coding sequences, for example, a second DNA sequence which is flanked by regulatory elements effective to allow expression of the sequence in plant cells. This second DNA sequence can encode any number of useful gene products including products useful to increase fruit sugar content, increase plant/fruit fungal resistance, increase plant/fruit viral resistance, and effective to reduce ethylene biosynthesis in fruit from the
10 plant.

Regulatory elements for use in the practice of the method of the present invention typically include transcriptional and translational initiation/termination signals. In one embodiment, the transcription regulatory elements include tissue or stage specific promoters, for example, tomato E4 (or E4-like) and tomato E8 (or E8-like). Promoters similar to,
15 for example, the E4 promoter can be identified for a plant of interest in order to employ a promoter system homologous to the explant cell type (*e.g.*, tomato promoters in tomato, raspberry promoters in raspberry, strawberry promoters in strawberry). Heterologous promoters are useful as well (*e.g.*, tomato-derived promoters in transgenic raspberries or in transgenic strawberries).

20 The present invention includes pure transgenic plants, in particular, pure transgenics generated by the method of the present invention. The present invention also includes transgenic plant products produced by the pure transgenic plants of the present invention. Such products include, but are not limited to, plant cells, seeds, calli, fruit, vegetables, flowers.

25 In one embodiment, the method of the present invention has been applied using explants from fruit-bearing plants, such as raspberry and strawberry. Transgenic plants can be isolated using the methods and materials described above. Accordingly, the invention further includes transgenic plants and products thereof, including transgenic fruit. Several embodiments of the present invention are as follows: transgenic red raspberry plants,
30 transgenic red raspberries, transgenic strawberry plants, and transgenic strawberries.

Transgenic fruit of the present invention can embody many modifications, including, but not limited to, increased sugar content, increased fungal resistance, increased viral resistance, and reduced ethylene biosynthesis. In one embodiment, reduced ethylene production is achieved by production, in the transgenic fruit, of a product effective to

accomplish such a reduction. Such products include, for example, S-adenosylmethionine hydrolase, aminocyclopropane-1-carboxylic acid (ACC) deaminase, ACC oxidase antisense molecule, ACC synthase antisense molecule, ACC oxidase cosuppression molecule, and ACC synthase cosuppression molecule.

- 5 These and other objects and features of the invention will be more fully appreciated when the following detailed description of the invention is read in conjunction with the accompanying drawings.

BRIEF DESCRIPTION OF THE FIGURES

- 10 Figure 1 illustrates the effect of SAMase expression on the methionine recycling pathway in plants;

- Figure 2A shows a flow chart outlining the construction of the *Agrobacterium tumefaciens* binary vectors used in the present study (pAG-1452 and pAG-1552). Figure 2B shows restriction maps of these vectors. The *EcoRI* and *HindIII* sites shown in pAG1452 are present at the same location in pAG1552. The agrobacterium Ti right and left borders are abbreviated B_R and B_L, respectively;
- 15

 Figure 3A represents petiole explants of red raspberry cv. Meeker with callus and shoot regenerants on regeneration medium with 30 mg/l hygromycin;

- Figure 3B illustrates shoot regenerants of red raspberry cv. Meeker on shoot proliferation medium with 15 mg/l hygromycin;
- 20

 Figure 3C shows transgenic clonal shoots of an event in cv. Canby;

 Figure 3D shows transgenic plant of cv. Meeker rooted on medium with 10 mg/l hygromycin, ready for outplanting to soil;

 Figure 3E shows stunted shoots from transformed regenerants of cv. Canby;

- 25 Figure 3F shows bud differentiation on leaf lamina of cv. Meeker;

 Figure 3G shows transgenic plants of cv. Meeker established in greenhouse;

- Figures 4A and 4B show Southern blots of DNA isolated from transgenic plants. In the figures, non-transformed Meeker (4A; lanes 2 and 14) and Canby (4B; lane 7) cvs. compared to DNA from independent transgenic lines in the same cultivars. DNAs were digested with either *EcoRI* alone (4A; lanes 2-13, 4B; lanes 1-6) or, in matching sequence, with both *EcoRI* and *HindIII* (4A; lanes 14-25, 4B; lanes 7-13). The blots were probed with a ³²P-labeled probe consisting of either SAMase and a putative raspberry ACC oxidase gene (4A) or with SAMase alone (4B). The blot shown in 4B was also probed with the SAMase/ACC-oxidase probe which resulted in the expected 1.4 kb band appearing in each
- 30

DNA track (not shown). Molecular weight markers in kb are shown along the left margins. Exposures were for 8 hours;

Fig. 5 shows restriction maps of *A. tumefaciens* binary vectors used as transformants. The *EcoRI* and *HindIII* sites indicated are present in the same location for both vectors pAG5520 and pAG5110. The agrobacterium right and left borders are abbreviated B_R and B_L, respectively;

Fig. 6 represents shoot regenerants of cultivar Tristar transformed with pAG5110. Leaves are shown with (a) blue and (b) non-blue regions, on treatment with X-Gluc;

Fig. 7 illustrates a cluster of shoots of cultivar Tristar transformed with pAG5110. The cluster contains both (a) completely blue shoots, and (b) shoots with some blue regions;

Fig. 8 shows leaf explants of cv. Totem undergoing shoot regeneration on selection medium containing 50 mg/l kanamycin. The non-transformed shoot on the right is bleached, indicating sensitivity to selection. The shoot on the left is resistant to selection and is green in color;

Fig. 9 shows explanted segments of a primary shoot regenerant of cultivar Totem on regeneration medium with 150 mg/l kanamycin. Segments capable of withstanding selection and capable of regeneration are indicated by arrows;

Fig. 10 shows rooted transgenic plants of cv. Totem on medium with 60 mg/l kanamycin, ready for outplanting to soil;

Fig. 11 shows transgenic plants of cv. Totem, established in greenhouse.

Figs. 12A-12C show Southern hybridization blots of transformed cv. Totem (pAG5520). In the figures, lane 1, untransformed Totem, is compared to DNA from nine independent transformation events (lanes 2-10). DNAs were digested with either *EcoRI* alone (Figs. 12A,C) or, in matching sequence, with both *EcoRI* and *HindIII* (Fig. 12B). The blots were probed with probes consisting of either SAMase alone (Figs. 12A,B) or with SAMase and a putative strawberry alcohol dehydrogenase gene (Fig. 12C); and

Fig. 13 is a flow chart outlining the transformation protocol for strawberry.

DETAILED DESCRIPTION OF THE INVENTION

30 I. DEFINITIONS

"Red raspberry" refers to the species *Rubus idaeus* L.

"Strawberry" refers to the species *Fragaria X ananassa*.

"Transformed explant" is explant tissue containing a mixture of transformed and non-transformed cells. Compare to "non-chimeric transgenic explant."

"Pure transgenic explant" or "Non-chimeric transgenic explant" is a plant that contains essentially only transformed cells, determined as follows. Explants with transformed cells are regenerated in the presence of a selection agent to form regenerated shoots. The regenerated shoots are divided into explants and the explants cultured under selective
5 conditions. If part of the explant tissue is susceptible to the effects of the selective agent, the explant tissue is considered to be chimeric, *i.e.*, containing both transformed and non-transformed cells.

Sensitivity to the selective agent is typically manifest by necrosis or bleaching of tissue excised from shoot regenerants where the excised tissue is grown under selective
10 pressure. Leaves, petioles, nodal and meristem segments of shoot regenerants are routinely tested. On the other hand, if no susceptible tissue is detected, then the source tissue is considered to be non-chimeric or pure transgenic.

"Pure transgenic plant" or "Non-chimeric transgenic plant" are plants regenerated from non-chimeric or pure transgenic explants.

15 "Plant shoots" are the first plant-like structures that outgrow from explant tissue cultured under regeneration conditions. The outgrowth is typically from a small number of cells present in the explant.

"Threshold concentration of selective agent" varies depending on the selective agent used and is determined by experimentation. The threshold concentration is the concentra-
20 tion of the selective agent that permits the growth of transformed cells carrying the selection gene, but which also allows either very low level (background growth) or no growth of non-transformed cells. The threshold concentration is typically the lowest concentration of selective agent that significantly inhibits the growth of non-transformed cells.

"Functional gene" is any gene introduced into plants that can express its encoded
25 sequences and produce the expected gene product, such as an RNA or protein, in the plant cells in which it resides.

"E4 promoter" as used herein is any promoter or regulatory sequence derived from a gene homologous to a tomato E4 gene.

30 II. TRANSFORMATION METHOD

The present invention includes an improved method for the generation of transformed plant cells and pure transgenic plants.

In the method of the present invention, a suitable expression vector is selected for introduction into the cells of the target explant. The expression vector typically has at least

one DNA sequence that encodes a gene encoding a selectable marker functional in plant cells. Such selectable markers are known to those of skill in the art and include the *hpt* gene (which confers resistance to the antibiotic hygromycin; *Klebsiella sp.*), and the *nptII* gene (originally obtained from TN5, having broad host range, conferring resistance to geneticin and kanamycin).

Expression of the selectable marker is typically under the control of a promoter that functions constitutively in plant cells (e.g., Pnos). Expression of the selectable marker gene produces a gene product that confers the ability of plant cells expressing the gene to grow in the presence of a selective agent (e.g., hygromycin).

Plant explants are typically the target of transformation. The expression vector can be introduced into the explant cells by a number of methods including electroporation, microinjection, and microprojectile bombardment. These methods are well known in the art (Klein, *et al.*; Miki, *et al.*; Bellini, *et al.*) and provide the means to introduce selected DNA into plant genomes.

In a preferred embodiment, the expression vector is an *Agrobacterium*-based vector and the transformation of the explant cells is carried out by co-culturing the explant in the presence of *Agrobacterium* carrying the expression vector. Numerous such *Agrobacterium* based vector systems are available to one of ordinary skill in the art (e.g., An, *et al.*, 1988; Becker, *et al.*, 1992). The use of one type of binary vectors in the practice of the present invention is described below in the Materials and Methods section.

Co-culturing of the explant and vector-bearing bacteria is typically carried out in liquid culture, under the conditions described below, for about 1 to 3 days. The concentration of the *Agrobacterium* in co-cultivation is typically between about 10^8 to about 10^9 transformed bacterial cells/ml of culture. In the examples described below the concentration is usually about $0.5-0.6 \times 10^9$.

After transformation of explant cells, the transformed explant cells are screened for the presence of the selectable marker gene by culturing the transformed explants in selective media having a threshold concentration of selective agent.

In the practice of the present invention, the ability of explants to regenerate is empirically evaluated. Having a robust regeneration system provides the maximum opportunity to recover transgenic plants from transformed explant cells. Some factors affecting regeneration ability include, but are not limited to, the following: media composition, hormone levels, concentration of selective agent, light levels, number of transfers to new culture media.

The ability to obtain regenerates from explants is maximized for the plant cells that are the selected transformation target. Different tissue explants may be transformed and the different tissues may require different regeneration conditions. In the method of the present invention, shoots, leaf, meristem and petiole explants were routinely used. For red
5 raspberry, petiole explants appeared to provide better callus production and shoot regeneration (Example 1, Table 1). For strawberry, leaf, meristem and petiole explants all provided good callus production and shoot regeneration.

One aspect of the present invention is the application of an iterative culture/selection method. In this method, when transformed explants demonstrate the ability to grow on
10 selection medium they are typically regenerated to form plant shoots, tissue explants isolated from the regenerated shoots, and the resulting explants grown on selection media at a higher concentration of selective agent than was present in the initial selection medium. The iterative culture selection method is continued providing increasingly stringent selection levels.

15 As described above, the threshold concentration of selective agent is determined. Typically, the first round of the iterative selection method is carried out at twice the threshold concentration, the second round at three times the threshold concentration, and so on. Any step-wise increase in selective agent concentration can be used, for example, 1X, 1.5X, 2X, 2.5X threshold concentrations.

20 Selective agent concentration is cultivar dependent and often explant tissue type dependent. In raspberry, for example, (Example 1) transformed explants of cv. Canby were subjected to geneticin selection as follows: petiole explants started at 5 mg/l went to 10, 15 then 20 mg/l, and leaf explants started at 10 mg/l and went to 15, 20, then 25 mg/l. Selective agent concentrations are typically in the range of 1-500 mg/l, but are, of course,
25 dependent on the agent, explant-type, and selectable marker used.

In another example, (Example 10) transformed strawberry explants of cv. Tristar were cultured in regeneration medium containing either 0, 10 or 25 mg/l kanamycin, followed by transfer to medium containing 50 mg/l, then subsequent transfer to medium containing 75 mg/l kanamycin.

30 The iterative culture method is repeated until pure transgenic explants are obtained. Pure transgenic explants are defined above. Briefly, a transformed explant that is the product of iterative selection is encouraged to undergo tissue regeneration, for example, by culturing the explant on shoot regeneration/proliferation medium. Explants are derived from the regenerated shoot(s), typically from leaf, meristem, nodal and petiole tissue. All

explant tissues are cultured on media usually containing the highest level of selective agent used in the iterative selection method.

The transgenic tissue is determined to be pure if all of the explants from regenerated shoots are maintained on the selective medium and show no signs of necrosis or bleaching
5 (extreme loss of chlorophyll).

When a pure transgenic explant is identified, the explant is regenerated to produce pure transgenic plants. The plants are then typically set in soil and allowed to mature for further evaluation.

Transgenic tissue is also evaluated by standard recombinant techniques to demon-
10 strate the presence of the introduced genes (*e.g.*, genomic DNA (Southern) hybridization analysis -- Materials and Methods and Examples 3, 8 and 11).

In practicing the method of the present invention, the concentration of the selective agent in the first round selection should be carefully selected to allow growth of the transformed cells, and typically low level or background growth of some non-transformed
15 cells. From this initial selection, the explant is usually subjected to shoot regeneration, leaf and petiole reselection, followed by a step-up selection (*i.e.*, increased concentration of selective agent). Callus development ensues. The callus is usually transferred to a new medium and then transferred to another step-up concentration of selective agent. Once again, shoot regeneration is carried out and the above procedure repeated at higher
20 concentrations of selective agent.

As an initial test of the purity of the transgenic, after shoot proliferation, leaf tissue is chopped up and placed in selection media. If part of the leaves are susceptible to the effects of the selection media (*e.g.*, necrosis or bleaching), then the tissue is likely not pure.

In addition to the selectable marker sequences, vectors used in the method of the
25 present invention typically have at least one second DNA sequence that encodes a functional gene. The functional gene is flanked by regulatory elements effective to allow expression of the sequence in plant cells (*e.g.*, transcription initiation/termination signals, translation initiation/termination signals).

Gene products which may be useful to express include functional genes encoding (i)
30 products affecting flavor or color modification proteins (*e.g.*, sucrose phosphate synthase, which may result in increased sugar content of fruit, (Worrell, *et al.*, 1991), (ii) products influencing plant and/or fruit fungal resistance (Toubart, *et al.*, 1992), (iii) products influencing plant resistance, (iv) enzymes, such as encoded by the taumatin gene, and (v) products that affect ethylene production, such as anti-sense or enzymes (*e.g.*, amino-

cyclopropane-1-carboxylic acid (ACC) deaminase, ACC oxidase antisense molecules, ACC synthase antisense molecules, ACC oxidase cosuppression molecules, and ACC synthase cosuppression molecules).

For example, in one embodiment of the present invention, a gene useful for the reduction of ethylene production is introduced into plants. One approach to reduce ethylene biosynthesis in plants and fruit utilizes a gene that encodes the enzyme S-adenosylmethionine hydrolase. This approach is described herein and in PCT International Application PCT/US90/07175, herein incorporated by reference.

The enzyme S-adenosylmethionine hydrolase, encoded by the *E. coli* bacteriophage T3, hydrolyses S-adenosylmethionine (SAM) to homoserine and 5'-methylthioadenosine (MTA) (Figure 1).

The enzyme is known by its recommended name, AdoMet hydrolase (AdoMetase), or by its other name, S-adenosylmethionine cleaving enzyme (SAMase) (Studier, *et al.*, 1976). Both products of the reaction (*i.e.*, homoserine and MTA) are recycled to methionine; MTA as previously shown (Figure 1) and homoserine via a metabolism pathway known to exist in plant tissues.

The AdoMetase gene has been identified, isolated, cloned, and sequenced from bacteriophage T3 (Hughes, *et al.*, 1987a; Hughes, *et al.*, 1987b; Studier, *et al.*, 1976). Other bacteriophages that encode the AdoMetase or SAMase genes are coliphage BA14, *Klebsiella* phage K11, and *Serratia* phage IV (Mertens, *et al.*; Horsten, *et al.*).

Different bacteriophages may be expected to contain AdoMetase genes with variations in their DNA sequences. The isolation of AdoMetase coding sequences from bacteriophage coding sequences can be accomplished as previously described for AdoMetase from bacteriophage T3. Alternatively, degenerative hybridization probes for AdoMetase coding sequences can be generated and used to screen plasmids carrying fragments of a selected bacteriophage's genome for the presence of homologous sequences. AdoMetase enzymatic activity can be evaluated by standard biochemical tests.

To increase the translational efficiency of the AdoMetase gene in plants, site directed mutagenesis of the nucleic acid sequences surrounding the ATG start codon was performed. The net effect of the substitutions change the CACCAAATGA in the native T3 sequence to GCCACCATGG which is an optimal eukaryotic translational initiation sequence (Kozak, *et al.*; Lutcke, *et al.*).

The change also introduces an *NcoI* site at the SAMase start codon which facilitates fusions to different promoters. The only alteration to the AdoMetase coding sequence is the

amino acid at amino acid position two which is changed from isoleucine to valine: this is a highly conservative amino acid change. The altered form of AdoMetase was named SAM-K (SEQ ID NO:1 and SEQ ID NO:2).

Previously described experiments (PCT International Application PCT/US90/-
5 07175), using transgenic plants expressing an AdoMetase gene and monitoring ethylene production, have demonstrated that the effect of AdoMetase on the pathway is to "short circuit" the branch that produces ethylene: ethylene production is reduced in such transgenic plants, including production in leaf tissue and fruit.

The regulatory regions used to guide expression of gene products can also be
10 obtained from a number of sources. Both constitutive and regulatable promoters are useful in the practice of the methods of the present invention. A tissue or stage specific promoter is a region of DNA that regulates transcription of the immediately adjacent (downstream) gene to a specific plant tissue or developmental stage of the plant or plant tissue. One exemplary regulatable promoter is the tomato E4 gene promoter (tomato E4 gene, SEQ ID
15 NO:4 and SEQ ID NO:5; tomato E4 gene promoter/Adometase, SEQ ID NO:6 and SEQ ID NO:7; Materials and Methods). Expression of the E4 gene has been shown to be induced (i) at the onset of ripening, and (ii) by treatment of tomatoes with ethylene (Lincoln, *et al.*, 1987; Lincoln and Fischer, 1988a, 1998b; DellaPenna, *et al.*, 1989). The E4/Adometase gene construct has been introduced into transgenic raspberries and into transgenic strawber-
20 ries using the methods of the present invention (see below).

The methods of the present invention are applicable to all higher plants, and particularly to fruit-bearing plants. The E4 promoter, and/or the transformed plant, may be selected from a variety of plants, including fruit-bearing plants, such as tomato, eggplant, legumes, raspberry, strawberry, melon, avocado, cherry, apricot, citrus fruits, etc.;
25 flowers, such as roses and carnations; and vegetables, such as cauliflower, and lettuce.

Regulatable promoters other than the E4 promoter can also be used in the practice of the present invention and include, but are not limited to the following: the E8 gene promoter from tomatoes (SEQ ID NO:3); polygalacturonase gene promoter from tomato; and the promoter for ethylene forming enzyme (EFE) from tomatoes. It is useful to restrict
30 expression of some genes to specific tissues, such as the fruit — for example, any gene that would be deleterious to the plant if it were expressed constitutively. Such genes would include genes which encoded degradative enzymes that deplete necessary metabolites.

Further, the tomato genes E4 and E8 can be used as hybridization probes against libraries of DNA representative of the genomes of other plant species. Identification of

homologous genes allows the identification of the regulatory sequences adjacent the homologous gene. Such regulatory sequences (*e.g.*, a promoter region) are then tested for tissue specific expression in the plant species from which they were isolated.

Using hybridization screening methods, an E4 homologue gene in raspberries has
5 been identified (SEQ ID NO:8 and SEQ ID NO:9). Using primers derived from these sequences, both the three and five prime ends of the raspberry E4 gene are isolated using the PCR rapid amplification of cDNA ends (PCR-RACE) reaction (Frohman, 1988, 1990), thus providing raspberry-derived promoter regions.

Additional raspberry E4 gene sequences were obtained by further hybridization
10 screening of raspberry genomic library clones. The sequence of a genomic copy of a raspberry E4 gene is presented in SEQ ID NO:10 (nucleotide sequence) and SEQ ID NO:11 (polypeptide sequence).

Such promoters, as well as the E4 promoter itself, can be tested for regulatable expression in heterologous plant systems using the methods described herein. A reporter
15 gene, such as *uidA* (Jefferson, *et al.*, 1986), which encodes GUS (β -glucuronidase), can be used to test tissue specific regulatable expression from these promoters. Expression of GUS protein can be easily measured by fluorometric, spectrophotometric or histochemical assays (Jefferson, 1987a, 1987b, 1989).

The transformation method of the present invention is applicable to essentially all
20 plants, including, but not limited to, fruit-bearing plants (*e.g.*, tomatoes, raspberries, strawberries and melons), vegetables (*e.g.*, cauliflower) and flowers (*e.g.*, carnations). One such example is strawberries. The generation of pure transgenic strawberries, from two Pacific Northwest cultivars of strawberry, is described herein.

The present method is particularly useful in the transformation of woody species,
25 that have historically had poor rates of transformation. When employing the transformation method of the present invention, transformation frequencies of woody species were greatly increased. One example of such a woody species is the red raspberry. The generation of transgenic raspberries, following the method of the present invention, is described below.

30 III. TRANSGENIC RASPBERRIES

Experiments performed in support of the present invention have yielded transgenic raspberry plants from a total of 218 independent transformation events (161 Meeker (MK), 4 Chilliwack (CH), 52 Canby (CY)). The transgenic plants have been established in soil for further evaluation of growth parameters an expression of the introduced traits.

Example 1 describes the growth response of *Agrobacterium* co-cultivated red raspberry explants when plated on media containing a selective agent. The cultivars were typically transformed with a binary vector in a disarmed *A. tumefaciens* strain. After co-cultivation, petioles and leaf explants were cultured on regeneration medium containing
5 selective agent.

Cultivar Meeker explants showed de-differentiation of cut leaves in 3-4 weeks. After 6 weeks (end of second transfer period) about 24.0% of the leaf and 33.3% of the petiole explants underwent shoot regeneration. With subsequent transfers the number of petiole explants that underwent shoot regeneration increased (Figure 3A; Table 1, Example
10 1).

The frequency of transformed cv. Meeker callus from both petiole and leaf explants was significantly higher than that of shoot regeneration and was capable of profuse growth in the presence of elevated levels of selective agent (relative to control explants). Typically, the percent recovery of transformed shoots was higher with petiole than with leaf explants.

15 Cultivar Chilliwack explants treated in similar fashion gave a transformation frequency of 0.9 and 0.7% from petiole and leaf explants, respectively, using the transformation method of the present invention (Example 1, Table 1).

Cultivar Canby was transformed with two binary vectors, pAG1552 and pAG1452, that each contain different selectable markers. Petiole and leaf explants after co-cultivation
20 with pAG1552 were cultured on selection medium with geneticin. The explants co-cultivated with pAG1452 were cultured on regeneration medium with hygromycin for petiole and leaf explants.

Petioles proved to be more efficient explants than leaves in all the cultivars independent of whether the selection agent was hygromycin or geneticin. Transformation
25 frequencies were obtained of 49.6% and 0.9% in the petiole and 15.9% and 0.7% in leaf explants for cultivars MK and CH respectively (Example 1). In cv. Canby the transformation rate ranged from 2.6-5.2% from petiole compared to 0.3-2.1% from leaf explants in different experiments.

In 3-4 weeks the cut edges of explants showed de-differentiation along with
30 spontaneous shoot regeneration in some of the explants. Most of the shoot differentiation took place over a period of 4 months of culture on selection medium.

The responses of four independent experiments in cv. Canby are summarized in Table 1. As in the other two cultivars, the number of explants which gave transformed

callus was significantly higher than the number of explants which gave rise to transformed shoots.

The *hpt* gene was found to be more efficient than *nptII* for recovering transformants. Experiments evaluating the different selection markers had shown that hygromycin and geneticin gave clear cut-off points compared to kanamycin in arresting the growth of raspberry tissue. Nevertheless, stable transgenic plants were obtained, at a frequency of 2.6-5.2% from petiole explants using the selection marker *nptII* gene. These results contradict the report of Graham, *et al.* (1990) that *nptII* gene is unsuitable as a selection marker gene for *Rubus*.

It was found that 50 mg/l kanamycin was inhibitory for organogenesis in *Rubus* and therefore, the transformants were raised in the absence of selection. It is possible that geneticin is a more effective antibiotic for *Rubus* than kanamycin although both antibiotics are aminoglycoside components that are detoxified by the neomycin phosphotransferase enzyme.

Frequency of shoot regeneration was higher with explants selected on medium with hygromycin while the frequency of transformed callus was higher with explants selected on medium with geneticin. Petiole explants gave higher rates of transformation both in terms of callus and shoot regeneration, irrespective of selection agent (Example 1, Table 1).

Transformed explants were periodically transferred to fresh media. From these samples, primary shoot regenerates were excised and individually cultured on shoot proliferation medium (Example 2) containing an appropriate selective agent. Upon transfer to such selective medium, the following four typical responses were observed:

- (a) complete necrosis of the shoot (non-transformed escape);
- (b) arrested shoot development with pale green leaves (non-transformed escape);
- (c) vigorous growth of single shoot (putative transformant); and
- (d) multiple shoot proliferation (putative transformant).

Putative transformants were further analyzed for the presence of non-transformed regions by transfer of explants to selective medium. The process of explant isolation and reculture on selection medium was repeated only when isolated tissue explants were capable of growth on selection medium. This process, the iterative culture method, is continued under increasingly stringent selection levels. Pure transgenic plants are identified when all test explant tissue is determined to be resistant to the appropriate selective agent. Trans-

genic shoots were cultured on proliferation medium with selection for generating clonal plants of each transformation event (e.g., Figure 3C).

The transformation method of the present invention employs a gradual increase in concentration of the selective agent, depending on tissue responses. Recovery of non-chimeral transgenics is valuable in plants, like raspberry, where the genetic constitution is maintained by vegetative means and recovery of pure transformants through seed segregation is not practical. However, since shoot meristems normally arise from more than one cell and also they need not arise from cells of clonal origin, the formation of chimeral plants is more of a rule than an exception in transformation experiments, particularly where plant regeneration occurs via organogenesis. This point was well-illustrated in recent reports on tobacco (Oono, *et al.*, 1993; Schmulling and Schell, 1993), flax (Dong and McHughen, 1993a; Dong and McHughen, 1993b) and melon (Dong and McHughen, 1991).

As discussed above, putative transformants of raspberry were subjected to several iterations of tissue isolation and reculture on higher stringency selection for recovering uniformly-transformed plants. Shoots from each of the independent transformation events went through this rigorous screening procedure before they were considered as transformed. The transformation frequencies reported here were calculated only after such testing procedure.

Genomic DNA was isolated from putative transgenic plants and analyzed to confirm the presence of the transgenes and to characterize the structure of the integrated DNA (Example 3).

Figures 4A and 4B show the results of Southern analyses of genomic DNA isolated from transgenic plants obtained by the method of the present invention. In general, a variety of integration patterns were detected including single, double, and triple insertions and multiple insertions at a single site (Example 3). The majority of the transgenic plants investigated have intact single or double integration events.

Gene copy number for the Adometase gene, introduced by transformation, were also determined (Figures 4A and 4B). Gene copy number of the Adometase gene was typically determined relative to a putative raspberry ACC oxidase (ACCO) gene. A clone containing the putative raspberry ACCO gene was obtained by hybridization screening of raspberry genomic DNA library (Novagen, Madison, WI) using a probe derived from the tomato ACCO gene sequence (Hamilton, *et al.*, 1991; Van der Straeten, *et al.*, 1990).

A rather complex pattern of integration structures is seen in the results presented in Figure 4B. It is interesting that these multiple integration patterns appear to be specific for the Canby cultivar and the *nptII* selectable marker gene.

Confirmed pure transgenic shoots (*i.e.*, where (i) all explants are resistant to the appropriate selective agent, and (ii) the gene of interest was demonstrated to be present by Southern hybridization analysis) were transplanted directly to soil or cultured on rooting media then transplanted to soil in order to grow complete transgenic plants (Example 4).

Occasional abnormalities were observed among the transgenic plants (Example 5), however, only transgenic plants having normal appearance were transferred to soil. Figure 3G shows exemplary transgenic plants established in greenhouse. These plants were indistinguishable from control non-tissue cultured plants.

The results presented above demonstrate the efficacious and reproducible generation of exemplary pure transgenic red raspberry plants.

IV. TRANSGENIC STRAWBERRIES

Experiments performed by the methods of the present invention have yielded about 500 transgenic strawberry plants from 250 independent transgenic events. The transgenic plants have been transferred to soil for further evaluation of growth parameters and expression of the introduced traits. A gene for the control of ethylene biosynthesis has been incorporated into strawberry (cultivar Totem) for the first time.

Examples 6 through 9 describe the general procedures utilized for co-cultivation, transformation, characterization, and rooting of two Pacific Northwest cultivars of strawberry, Tristar and Totem. As described in Example 10, cultivar Tristar was transformed with disarmed strains of *Agrobacterium tumefaciens* (*A. tumefaciens*), LBA4404 or EHA101, containing a binary vector with marker genes *uidA* and *nptII*.

Cultivar Totem was transformed with *A. tumefaciens* strains EHA101 or EHA105 harboring binary vectors with selectable marker genes *nptII* or *hpt* and with a gene for S-adenosylmethionine hydrolase (SAMase) for control of ethylene biosynthesis (Example 11). As shown in Table 2, the frequency of transgenic shoots in cultivar Totem ranged from 12.5% to 58.8% of the original treated explants when using plasmids containing the gene encoding SAMase.

Primary shoot regenerants obtained on selection medium were subjected to several iterations of tissue isolation and reculture on higher stringency selection medium to achieve recovery of uniformly transformed plantlets. Transgenic strawberry plants were confirmed

by their ability to undergo rooting on medium with selection at 60 mg/l kanamycin or 10 mg/l hygromycin.

Greater than 95% of the transformation events from different experiments were capable of profuse rooting in the presence of selection agent, as described in greater detail

- 5 in Example 11. Insertion of the SAMase gene and its integration into the strawberry genome were confirmed by Southern hybridization.

The results presented herein demonstrate the efficacious and reproducible generation of exemplary pure transgenic strawberry plants.

10 V. UTILITY

A. THE TRANSFORMATION METHOD OF THE PRESENT INVENTION

- The transformation frequency obtained by the method of the present invention is the highest that has been obtained for *Rubus* species or for any other woody fruit crops. It is also to be noted that the regenerants and callus from one explant were treated as one event
15 although it is possible to have more than one transformation event per explant. This implies that the actual transformation efficiency is even higher than the figures reported herein. The more conservative figure was used to avoid possible errors in separating independent events.

- The transformation method of the present invention, provides a high efficiency
20 transformation system for plants in general and also means to generate pure (or non-chimeric) transgenic plants. The ability to recover a large number of transgenic events is important for the purpose of field testing of transgenic plants, in view of the typical development of somaclonal variants and variations in transgene expression due to gene copy number and positional effect.

- 25 The transformation method of the present invention was also used to incorporate, for the first time, a gene controlling ethylene biosynthesis into the strawberry cultivar Totem. Transformation efficiency ranged from 12% to nearly 60%.

- The method of the present invention provides a high rate of transformation frequency and generation of pure transgenic plants. Examples are described herein for strawberry
30 and red raspberry. Red raspberry (*Rubus idaeus* L.) has historically been recalcitrant to molecular genetic manipulations.

B. TRANSGENIC FRUIT: RED RASPBERRIES AND STRAWBERRIES

Increased fruit firmness is a component of reduced susceptibility to fruit rot, a major factor in the extension of fresh market shelf life (Daubeney and Anderson, 1993). Controlling the metabolic processes which cause ripening has the potential to improve shelf life, extend the harvest season and the market area for highly perishable or easily damaged fruits.

Transgenic tomatoes with increased firmness and pronounced delay in ripening were obtained by incorporating a gene for S-adenosylmethionine hydrolase (see above). Adometase catalyses the conversion of S-adenosylmethionine (SAM) to methylthioadenosine (MTA) and homoserine which can reenter the methionine recycling pathway (Figure 1). SAM is therefore not available for the synthesis of aminocyclopropane-1-carboxylic acid (ACC), the metabolic precursor for ethylene synthesis. Transgenic tomatoes with the Adometase gene, which are now undergoing field trials, showed a greatly-reduced ability to synthesize ethylene and significantly increase post-harvest shelf-life.

Ethylene is reported to play a major role in the ripening and abscission of raspberry fruit (Sexton, *et al.*, 1993). Perkins-Veazie, *et al.* (1992) observed that a dramatic increase of ethylene production during the fruit ripening of raspberry. The Adometase gene has now been incorporated into red raspberry cultivars in order to test the efficacy of the gene to reduce softening and increase the shelf-life of berries.

Although strawberry is not considered a typical climacteric fruit (Kader, 1991), there is evidence that indicates that the removal of ethylene may also play a role in reducing spoilage of fresh berries such as strawberries. Exogenous application of ACC (the immediate metabolic precursor to ethylene), to 'Earlyglow' strawberry at preclimacteric and climacteric stages induced higher ethylene production while AVG (ethylene antagonist) application inhibited the biosynthesis of ethylene (Basiouny, 1989).

Treatment of strawberry cv. Chandler with ethylene absorbent gave increased firmness combined with reduced fungal attack (De la Plaza and Merodia, 1989). The SAMase gene has also been introduced into a Pacific Northwest variety of strawberry, cultivar Totem, to examine the efficacy of the gene to reduce softening and increase the post-harvest life of strawberries.

Transgenic fruit, such as transgenic raspberries and strawberries can also be generated containing other functional genes that affect fruit and plant characteristics, for example, the following:

- (i) increased sugar content of fruit;

- (ii) increased fungal and/or viral resistance of plants and/or fruit; and
- (iii) reduced ethylene biosynthesis.

The following examples illustrate, but in no way are intended to limit the present
5 invention.

MATERIALS AND METHODS

A. EXPLANT SOURCE

Leaves, meristematic tissue and petioles were excised from proliferating shoot
10 cultures maintained on modified MS medium (Murashige and Skoog, 1962) supplemented
with 1 mg/l benzylaminopurine (BA) and gelled with 0.2% phytigel. Typically, the
following tissue sources were not used for explant isolation: leaves and petioles from the 2-
3 nodes close to the shoot tip, and leaves of greater than 10 mm in size.

Petioles were cut into 4-6 mm segments. Leaf blades 4-5 mm in length were used
15 as whole explants or they were cut into transverse halves when blades were greater than 6
mm in size.

Leaf explants were cultured with the adaxial surface in contact with the medium.

Meristematic tissue was obtained by excision of 10-12 mm sections of the actively
proliferating base of 3-4 week old strawberry plants maintained *in vitro* on propagation
20 medium. These sections typically contained the apical meristem region from several shoot
buds.

B. BACTERIAL STRAIN AND BINARY VECTORS

Agrobacterium tumefaciens strain EHA105 contained the disarmed super-virulent
25 plasmid pTiBo452 in the C58 chromosomal background (Hood, *et al.*, 1993).

The plasmid vectors containing the S-adenosylmethionine hydrolase (Adometase or
SAMase) gene (were constructed using the backbone of pGPTV binary vectors (Becker, *et al.*, 1992) where the marker genes had been divergently organized for efficient expression
and could be easily removed or replaced.

30 The AdoMetase gene was identified on an *AluI-HaeIII* restriction fragment from
purified T3 DNA (Hughes, *et al.*, 1987a). Bacteriophage T3 is available under ATCC No.
11303-B3 (American Type Culture Collection, 12301 Parklawn Dr., Rockville MD
20852). The DNA fragment was first cloned into the bacteriophage M13 MP8 vector
(Pharmacia LKB Biotechnology, Inc., Piscataway, NJ). A *MaeIII* to *BamHI* fragment was

subcloned into the pUC19 plasmid vector (Pharmacia) to produce pUC19-AdoMetase. This vector was transformed into *E. coli* and used as a source of Adometase DNA.

The constructions of vectors pAG-1452 and pAG-1552 are shown schematically in Figure 2A. A 1.18 kb tomato E4 promoter containing fragment was generated using E4-specific polymerase chain reaction primers (Cordes, *et al.*, 1989) containing *Hind*III and *Nco*I cleavage sites. The promoter sequences were cloned adjacent the 5' end of the Adometase gene (Figure 2A, pAG-117). The sequence of the E4 promoter/Adometase gene construct is presented as SEQ ID NO:6.

A 1.7 kb fragment, containing the E4 promoter and Adometase coding sequences, was obtained from pAG-117 by *Eco*RI/Mung Bean nuclease/*Hind*III digestion. This fragment was cloned into the *Sac*I/Mung Bean Nuclease/*Hind*III sites of the vectors pGPTV-*hpt* and pGPTV-*npt*II (Figure 2A).

The binary vector, pAG1452 had the *hpt* gene for resistance to the antibiotic hygromycin under the *nos* promoter located near the left border and the SAMase gene driven by the tomato E4 promoter (Gamborg, *et al.*, 1968) located near the right border (Figures 2A and 2B).

The binary vector pAG1552 differed from pAG1452 by having the *npt*II marker gene in place of the *hpt* gene (Figures 2A and 2B).

20 C. CO-CULTIVATION OF EXPLANTS WITH AGROBACTERIUM

A freshly-grown single colony of *Agrobacterium* was inoculated into 30 ml of MG/L (Garfinkel and Nester, 1980) liquid medium supplemented with 50 μ M acetosyringone, pH. 5.6, was grown on a shaker at 200 rpm for overnight (16-18 hours). The bacterial suspension had an average count of $0.5-0.6 \times 10^9$ cells/ml at the start time of co-cultivation with plant tissues.

The petioles and leaf explants soon after excision were soaked in *Agrobacterium* suspension. After 30-60 minutes, these were transferred to flasks containing liquid medium of composition-modified MS (Murashige and Skoog, 1962) salts, B5 (Gamborg, *et al.*, 1968) vitamins, 2 mg/l glycine, sucrose 3%, 1-4 mg/l BA, 0.2 mg/l IAA and 50 μ M acetosyringone, pH 5.6, and kept on shaker at 100 rpm. The density of explants is about 100-120 segments in about 30 ml of medium in 125 ml flasks.

The next day, the medium was decanted and replaced with fresh liquid medium of the same composition and kept on the shaker. After 2 days of co-cultivation, the explants

were rinsed with liquid medium without acetosyringone, blotted and plated on regeneration medium containing a selection agent (*e.g.*, kanamycin, G418 - geneticin, or hygromycin).

At the end of co-cultivation period if the suspensions turned visibly cloudy with *Agrobacterium* growth, the explants were incubated with liquid medium, supplemented with
5 500-1000 mg/l cefotaxime for one hour on the shaker before blotting and plating on screening medium.

D. TISSUE CULTURE MEDIUM AND GROWTH CONDITIONS

The shoot regeneration/proliferation medium consisted of MS (Murashige and
10 Skoog, 1962) salts, B5 (Gamborg, *et al.*, 1968) vitamins, 2 mg/l glycine sucrose 3%, supplemented with IBA 0.1 mg/l, 0.1-1.0 mg/l TDZ and 10 mg/l silver nitrate.

For cultivar Meeker, 3% sucrose was replaced by 3% D-glucose as the carbon source. The pH of the medium was adjusted to 5.8 before gelling with 0.2-0.25% phytigel.

15 The culture medium was autoclaved at 120°C at 1.1 kg.cm⁻². The antibiotics and silver nitrate which were filter sterilized and added as the media cooled. Depending on the plasmid strain the regeneration medium contained antibiotics carbenicillin (500 mg/l) and geneticin (3-25 mg/l) or hygromycin (10-30 mg/l) for screening of transformed shoots.

Cultures were kept at 25°C with 16-hour photo-period provided by white fluores-
20 cent light at an average intensity of 50 $\mu\text{mol m}^{-2} \text{ s}^{-1}$. Observations were recorded every 3-4 weeks and cultures were transferred to fresh medium of the same composition with appropriate changes in the level of antibiotics.

Soon after co-cultivation the explants received the lowest level of selection (threshold concentration of the selection agent). The concentration for the initial selection was
25 typically a media concentration of the selective agent that was able to essentially prevent the growth of the corresponding non-transformed cultivar (*e.g.*, non-transformed Meeker as a control for transformed Meeker).

As the explants underwent proliferation in culture, the selection level was gradually increased based on the rate of dedifferentiated tissue on the explant. The selection level
30 was elevated to a maximum of 25 mg/l of geneticin or 30 mg/l hygromycin in the case of explants with prolific callus growth.

Putatively transformed red shoot regenerants were isolated and cultured on shoot proliferation medium with selection at 14-20 mg/l of geneticin or hygromycin. Rooting medium for transgenic shoots contained half MS (Murashige and Skoog, 1962) salts, B5

vitamins (Gamborg, *et al.*, 1968), 3% sucrose (or D-glucose for cv. Meeker), 0.05 mg/l IBA, 300 mg/l carbenicillin and 10 mg/l hygromycin or geneticin.

Leaf, petiole and nodal explants were cultured in petri plates with 40 ml of regeneration/proliferation medium. Typically, there were 20 petiole segments and 10 leaf segments per plate. Shoot explants (6-9) for multiplication/rooting were cultured on phytatrays with 120 ml of the proliferation or rooting medium.

E. TREATMENT OF PRIMARY SHOOT REGENERANTS AND RECOVERY OF TRANSGENIC CLONES

Shoot regenerants were isolated and cultured on shoot proliferation medium containing 15-20 mg/l geneticin or hygromycin. Leaves, petioles and nodal segments were isolated from shoots which withstood selection, and cultured on regeneration or proliferation medium with 20 mg/l geneticin or hygromycin. This iterative process of reculture of excised tissues from regenerants was continued until no part of the shoots necrosed or bleached under selection pressure ("bleaching" is loss of significant amounts of chlorophyll).

Shoots were considered as fully transformed (*i.e.*, non-chimeric or pure) only after they passed the above criteria. Such shoots were multiplied on proliferation medium for generating clonal plants derived from different transformation events. Tissue samples from such plants were used for molecular confirmation of transformation events.

F. TRANSFORMATION EFFICIENCY

Frequency of transformation was defined as "the number of explants that gave antibiotic resistant callus and/or shoot regenerants" relative to "the total number of co-cultivated explants." Transformation frequency was expressed in percentage points.

G. ESTABLISHMENT OF TRANSGENIC SHOOT/PLANTS IN THE GREEN HOUSE

Individual shoots were isolated from profusely proliferating shoots, growing on selection medium, for root induction or were transferred directly to soil.

For direct transfer to soil, the shoot base was dusted with rooting mix (Hormex powder #3) before placing in potting mix. Phytatrays with rooted plants were kept in the greenhouse with loosened lids for 2-4 days, followed by transfer to soil after rinsing off the media with water.

H. GENOMIC DNA HYBRIDIZATION ANALYSIS

Genomic DNA was isolated from leaf tissue of transgenic and non-transformed control plants following the method of Dellaporta, *et al.* (1983). The DNA was digested with either *EcoRI* or *EcoRI* and *HindIII*, the restriction digestion fragments electrophoretically separated, transferred to a nylon membrane (Oncor, Gaithersburg, MD),
5 hybridized with ³²P radiolabeled probes and autoradiographed using standard procedures (Sambrook, *et al.*, 1989; Ausubel, *et al.*).

The hybridization probes used were a 550 bp fragment containing the SAMase gene or a 1050 bp fragment containing the genes for SAMase and a putative raspberry aminocyclopropane-1-carboxylic acid oxidase (ACCO) gene (obtained by hybridization of a
10 tomato ACCO gene-specific probe (Hamilton, *et al.*, 1991; Van der Straeten, *et al.*, 1990) to a library of raspberry genomic DNA (Novagen)). Transgene copy number was estimated by comparing the ACCO and SAMase band intensities using a high-resolution flat bed scanner and the "NIH-Image" image analysis program on an Apple MacIntosh Computer.

15

EXAMPLE 1

RESPONSE OF CO-CULTIVATED RASPBERRY EXPLANTS ON SELECTION MEDIUM

A. CV. MEEKER

20 Cultivar Meeker was transformed with the binary vector pAG1452 in the disarmed *A. tumefaciens* strain EHA105. After co-cultivation, petioles and leaf explants were cultured on regeneration medium with 10 mg/l hygromycin. In 3-4 weeks de-differentiation of cut leaves was observed. At the end of the second transfer period (6 weeks), about 24.0% of the leaf and 33.3% of the petiole explants underwent shoot regeneration.

25 The number of petiole explants undergoing shoot regeneration (Fig. 3A) increased with subsequent transfers. The petiole explants gave 49.6% shoot regeneration at the end of 4 months of culture on selection medium (Table 1).

TABLE 1

FREQUENCY OF TRANSFORMATION OBTAINED IN RED
RASPBERRY CVS. MEEKER, CHILLIWACK, AND CANBY

| Cultivar | Expt ID | Plasmid | Explant | # Initial Explants | Transformation Frequency % | | No. of Events in Soil |
|------------|---------|---------|----------|--------------------|----------------------------|------------|-----------------------|
| | | | | | Callus | Shoot Regn | |
| Meeker | RT18 | pAG1452 | Petiole | 244 | 74.1 | 49.6 | 88 |
| | | pAG1452 | Leaf | 675 | 31.3 | 15.9 | 73 |
| Chilliwack | RT18 | pAG1452 | Petiole* | 214 | 37.0 | 0.9 | 2 |
| | | pAG1452 | Leaf* | 430 | 14.4 | 0.7 | 2 |
| Canby | RT24 | pAG1552 | Petiole | 467 | 91.4 | 2.6 | 10 |
| | | pAG1552 | Leaf | 314 | 0.3 | 0.3 | 1 |
| Canby | RT25 | pAG1552 | Petiole | 190 | 95.8 | 3.7 | 4 |
| | | pAG1552 | Leaf | 223 | 9.4 | 0 | 0 |
| Canby | RT28 | pAG1552 | Petiole | 308 | 66.9 | 5.2 | 5 |
| | | pAG1552 | Leaf | 322 | 43.5 | 3.1 | 8 |
| Canby | RT27 | pAG1452 | Petiole | 308 | 51.6 | 8.1 | 19 |
| | | pAG1452 | Leaf | 288 | 30.6 | 2.4 | 6 |

Note: Culture period 120 to 125 days.

* ~ 50% explants lost due to contamination.

The shoot regeneration frequency of leaf explants decreased to 15.9% at the end of 4 months culture since many of the early regenerants underwent complete necrosis (Fig. 3B) after transfer to proliferation medium with hygromycin. Frequency of transformed callus from both petiole and leaf explants was significantly higher than that of shoot regeneration and was capable of profuse growth in the presence of 30 mg/l hygromycin.

Control leaf and petiole explants did not withstand even 10 mg/l hygromycin and were completely necrosed by the second culture period. The percent recovery of transformed shoots was higher with petiole than with leaf explants.

B. CV. CHILLIWACK

As shown in Table 1, cv. Chilliwack treated with *A. tumefaciens* strain EHA 105 containing the binary vector pAG1452, gave a transformation frequency of 0.9 and 0.7% from petiole and leaf explants respectively. Initially 25% of the petiole and 9.8% leaf explants underwent shoot regeneration during 4-6 weeks culture on

regeneration medium with selection at 10 mg/l hygromycin. But many of these initial shoot regenerants necrosed upon excision and culture on proliferation medium with the addition of selective agent. In addition, many of the leaf explants appear to have been lost due to hypersensitivity to *Agrobacterium* during the co-cultivation period.

C. CV. CANBY

Cultivar Canby was transformed with both binary vectors, pAG1552 and pAG1452. Petiole and leaf explants after co-cultivation with pAG1552 were cultured on selection medium with geneticin 5 and 10 mg/l geneticin, respectively. The explants co-cultivated with pAG1452 were cultured on regeneration medium with 10 and 20 mg/l hygromycin for petiole and leaf explants, respectively.

In 3-4 weeks the cut edges of explants showed de-differentiation along with spontaneous shoot regeneration in some of the explants. Most of the shoot differentiation took place over a period of 4 months of culture on selection medium.

The responses of four independent experiments in cv. Canby, three with plasmid pAG1552 and one with pAG1452 are summarized in Table 1. As in the other two cultivars, the number of explants which gave transformed callus was significantly higher than the number of explants which gave rise to transformed shoots. The transformed callus grew uninhibited at 25 mg/l geneticin or 30 mg/l hygromycin depending on the transgene *nptII* or *hpt* while growth of control non-transformed tissues was completely inhibited at much lower concentrations, 5-10 mg/l.

Frequency of shoot regeneration was higher with explants selected on medium with hygromycin while the frequency of transformed callus was higher with explants selected on medium with geneticin. Petiole explants gave higher rates of transformation both in terms of callus and shoot regeneration, irrespective of selection agent.

EXAMPLE 2

TREATMENT OF PRIMARY RASPBERRY SHOOT REGENERANTS
AND RECOVERY OF TRANSGENIC CLONES

During the periodic transfer of leaf and petiole explants to fresh medium, the differentiated shoots, about 10-15 mm in size, were excised and individually

cultured on shoot proliferation medium with 15-20 mg/l geneticin/hygromycin depending on the strain pAG1452 or pAG1552 used in the experiment.

Mainly four types of responses were observed: (a) complete necrosis of the shoot; (b) arrested shoot development with pale green leaves; (c) vigorous growth of single shoot; and (d) multiple shoot proliferation. Among these, the first two categories were considered as non-transformed escapes or with very few transformed cell population and discarded. Vigorously-growing single-shoot and multiple-shoots were considered putative transformants and used for further analysis to check whether the whole shoot was uniformly transformed.

Leaves, petioles, and nodal explants of the primary regenerants were excised and cultured on regeneration/proliferation medium with 20 mg/l of the selection agent geneticin/hygromycin. The majority of the explants underwent callusing and shoot regeneration, or bud growth in the case of nodal segments, while some of the explants necrosed and responded like corresponding control, non-transformed tissues on selection.

When the presence of such non-transformed regions were identified in the putative transformants, the process of explant isolation and reculture on selection medium was repeated only when isolated tissue explants were capable of growth on selection medium. Transgenic shoots were then cultured on proliferation medium with selection for generating clonal plants of each event (Figure 3C).

EXAMPLE 3

GENOMIC DNA HYBRIDIZATION ANALYSIS OF TRANSGENIC RASPBERRY PLANTS

DNA isolated from putative transgenic plants were subjected to DNA hybridization (Southern) analysis to confirm the presence of the transgenes and to characterize the structure of the integrated DNA.

Plant genomic DNA was isolated and evaluated as described above. The DNA was digested with *EcoRI* alone or in conjunction with *HindIII*. *EcoRI* cleaves the region between the borders of the binary vector once and therefore produces junction fragments that can be recognized by hybridization of cleaved DNA with an Adometase probe (Figure 2B). Junction fragments can provide information on the transgene copy number and the number of independent integration events.

The *EcoRI/HindIII* double digest produces a single fragment internal to the T-DNA borders that can be also be detected using an Adometase hybridization probe.

Figures 4A and 4B show the results of Southern analyses of genomic DNA isolated from transgenic cv. Meeker with pAG-1452, and cv. Canby with pAG-1552, respectively. In general, a variety of integration patterns were detected including single, double, and triple insertions and multiple insertions at a single site.

Figure 4A, lanes 3 to 13, show the junction fragments from eleven transgenic events in cv. Meeker. Most are single integration events with one double (lane 5) and one triple (lane 7) event. Lane 8 is aberrant due to the unusually faint bands and the observation that one band is smaller than the predicted 4.2 kb *EcoRI* to left border fragment size of pAG-1452 (see Figure 2B). Lanes 9 and 10 contain faint, single copy bands.

In Figure 4B, the *EcoRI* digested DNA produced bands that seem to fall into two intensity categories suggesting a complex integration structure.

Estimates of the SAMase gene copy number were also made using a hybridization probe consisting of both the SAMase gene and a putative raspberry ethylene-forming enzyme gene or ACC oxidase (ACCO) which has one allele. The ACCO probe produces a band intensity equivalent to two copies of the gene. It also serves to confirm that the DNA has been completely digested by *EcoRI* and provides a measure of the relative amounts of DNA in each lane.

Because the ACCO and SAMase genes are on a single plasmid from which the double hybridization probe is made, the intensity differences between the *EcoRI/HindIII* SAMase bands and the EFE bands can be compared and were used to quantitate the SAMase gene copy number.

In Figure 4A there is good agreement between the number of integrations predicted by the junction fragment analysis and the intensity of the *EcoRI/HindIII* SAMase bands.

In Figure 4B the copy number estimation places limitations on the possible integration structures predicted by the *EcoRI* pattern. One line had multiple integrations (see Figure 4B, lanes 6 and 13) estimated at greater than 20 copies of the SAMase gene.

EXAMPLE 4

ROOTING AND TRANSPLANTATION OF TRANSGENIC RASPBERRY SHOOTS

Individual shoots isolated from multiple shoot complex were cultured on rooting medium with selection at 10 mg/l geneticin or hygromycin (Figure 3D).

5 All the rooted shoots were successfully transplanted to soil. When shoots were directly transplanted to soil from proliferation medium, the survival rate was typically 60-70%.

EXAMPLE 5

OCCASIONAL ABNORMALITIES AMONG RASPBERRY TRANSGENICS

10 In cultivar Canby (RT24 experiment, Table 1) one of the events gave bristle type shoots on regeneration medium. These shoots were stunted in appearance and had limited expansion of leaf lamina (Figure 3E).

15 In cv. Meeker an interesting kind of shoot regeneration was observed occasionally on leaves of some of the transgenic shoots. Shoot buds arose from all over the adaxial surface of leaves still attached to the shoots growing in proliferation medium with selection. If these leaves were detached and placed on the same shoot proliferation medium, the shoot buds developed into shoots (Figure 3F). This phenomenon was not observed in the control non-transformed proliferation
20 cultures while stunted and bristle type shoots were occasionally observed among the control regenerants.

Only transgenic plants having normal appearance were transferred to soil. Figure 3G shows transgenic plants established in greenhouse. These plants were indistinguishable from control non-tissue cultured plants.

25

EXAMPLE 6

EXPLANTS AND CULTURE CONDITIONS FOR STRAWBERRY CULTIVARS

The explants source was provided by three to four week old cultures of the strawberry cultivars, Tristar and Totem, maintained *in vitro* on propagation
30 medium. The propagation medium contained the following: basal medium (Murashige and Skoog, 1962), 1 mg/l indoleacetic acid (IAA), 1 mg/l benzyl-aminopurine (BA), and 0.01 mg/l gibberellic acid (GA); maintained at pH 5.8, and gelled with 0.8% agar (Sigma A1296).

Meristematic sections (10-12 mm) of the actively proliferating base of cultivar Tristar explants (containing several shoot buds) were co-cultivated with *A. tumefaciens*. Co-cultivation of cultivar Totem explants with *A. tumefaciens* was carried out using either leaf or petiole tissues from the explant, or whole young shoots (5-7 mm in length), segmented into 2-3 mm pieces. Cultivar Totem petioles were cut into 4-6 mm sized sections prior to co-cultivation. Folded young leaves explants (4-6 mm in length) were cut longitudinally and cultured with the adaxial surface in contact with the propagation medium.

Leaf, petiole and shoot base explants were cultured in petri plates (Nalgene, 100 x 25mm) containing 40 ml medium. Each petri plate contained 20-25 explant segments. Shoots for proliferation or rooting were cultured in "PHYTATRAYS II" (Sigma) containing 120 ml medium and from 9-10 shoots per tray.

All media components were autoclaved at 120°C at 1.1 kg cm⁻², with the exception of the antibiotics, acetosyringone and silver nitrate, which were filter sterilized prior to addition to the medium. All experimental and stock cultures were maintained at 25°C with 16 hour photoperiods provided by cool white fluorescent lamps at an average intensity of about 15-20 $\mu\text{molm}^{-2}\text{s}^{-1}$. Observations were recorded every 3-4 weeks followed by transfer to fresh medium.

EXAMPLE 7

TRANSFORMATION OF STRAWBERRY EXPLANTS

A. PREPARATION OF BACTERIAL SUSPENSIONS

A freshly grown single colony of *A. tumefaciens* (LBA4404, EHA101 or EHA105) was inoculated into 30 ml of MG/L (Garfinkel and Nester, 1980) liquid medium supplemented with 50 μM acetosyringone, pH 5.6, and grown on a shaker overnight (16-18 hours, 200 rpm). The resulting bacterial suspension had an average count of $0.5\text{-}0.6 \times 10^9$ cells/ml at the start time of co-cultivation with plant tissues.

B. BACTERIAL STRAINS AND BINARY VECTORS

Disarmed *A. tumefaciens* strains, LBA4404, EHA101 and EHA105, were used for strawberry transformation (Hood, *et al.*, 1994).

The binary vectors, pAG5110 and pAG5520, were derived from pGA482 (An *et al.*, 1985). The binary vector, pAG5110, contained DNA sequences encoding

both the *uidA* gene under the transcriptional control of the CaMV35S promoter, and the *nptII* gene, under the transcriptional control of the nopaline synthase (nos) promoter. The plasmid vector, pAG5520, contained the SAMase gene with the tomato fruit specific E4 promoter (Cordes et al., 1989) and the *nptII* gene, under the transcriptional control of the nos promoter (Fig. 5). The binary vectors, pAG1552 and pAG1452, were constructed using the backbone of the pGPTV binary vector (Becker et al., 1992). The vector constructs contained the SAMase gene driven by the E4 promoter (Cordes et al., 1989) located near the right border and the marker gene *nptII* (pAG1552) or *hpt* (pAG1452) under the nos promoter located near the left border (Fig. 2B).

C. CO-CULTIVATION WITH *A. TUMEFACIENS*.

Shortly following excision, isolated explants, as described in Example 6, were soaked in *A. tumefaciens* suspension. After 60-90 minutes, the explants were blotted on sterile filter paper and transferred to flasks containing liquid culture medium of MS basal salts (Murashige and Skoog, 1962), B5 (Gamborg et al., 1968) vitamins, 3% sucrose, 2 mg/l BA, 0.5 mg/l IAA, 50-100 μ M acetosyringone, pH 5.6, gelled with 0.25% "PHYTAGEL".

After 2 days of co-cultivation, the explants were rinsed with fresh liquid medium lacking acetosyringone, and incubated in flasks containing liquid medium supplemented with 500-1000 mg/l cefotaxime. The explant-containing flasks were placed on a shaker for 1 hour (100 rpm) before blotting the explants and plating on screening medium containing a selection agent.

D. SCREENING MEDIUM FOR SELECTION OF TRANSFORMANTS

The screening medium consisted of MS (Murashige and Skoog, 1962) salts, B5 (Gamborg et al., 1968) vitamins, 3% sucrose, 0.1-0.2 mg/l IBA, 5-10 mg/l BA, 500 mg/l carbenicillin (Gemini Bio-Products, Inc., Calabasas, CA) and one of the following selection agents: kanamycin (Sigma, St. Louis, MO), geneticin (Gibco, Gaithersburg, MD) or hygromycin (Calbiochem, San Diego, CA).

The initial selection levels of antibiotic were determined from the tolerance of non-transformed control tissue to the antibiotic selection agents. The concentration for the initial selection was typically a media concentration of the selection agent

that was able to essentially prevent the growth of the corresponding non-transformed cultivar.

Shortly following co-cultivation, the segmented explants were exposed to 25-50 mg/l kanamycin, depending upon the plasmid (pAG5110, pAG5520, pAG1552) and the cultivar. As the explants underwent proliferation during the subculture interval of 3-4 weeks, the selection levels were gradually increased. The selection level was elevated to a maximum of 200 mg/l kanamycin in the case of shoot proliferation medium for the maintenance of transformants (Fig. 13). The antibiotics kanamycin, geneticin (pAG5520) and hygromycin (pAG1452), were used as selection agents for cultivar Totem. The initial selection concentration of geneticin was 15 mg/l, elevated in a stepwise manner to a maximum of 40 mg/l. In the case of hygromycin, the initial concentration of selection agent was 10 mg/l, raised to a final level of 70 mg/l for maintenance of transformed shoots.

A portion of the explants in experiments ST10-ST14, as described in Example 11 and shown in Table 2, were cultured on screening medium containing 3-5 mg/l silver nitrate in order to evaluate the effects of silver nitrate on recovering transformants.

EXAMPLE 8

CHARACTERIZATION OF STRAWBERRY TRANSFORMANTS

A. HISTOCHEMICAL ASSAY FOR UDA EXPRESSION

Intact shoots (5-8 mm) and cut segments of the regenerants were subjected to 5-bromo-4-chloro-3-glucuronic acid (X-Gluc) treatment (Jefferson et al., 1987).

B. SOUTHERN HYBRIDIZATION

DNA isolated from transgenic and non-transformed strawberry plants were subjected to Southern hybridization analysis to confirm the presence of transgenes and to characterize the structure of the integrated DNA.

Genomic DNA was isolated from leaf tissue of transgenic and non-transformed control plants, as well as from greenhouse established plants (Doyle, *et al.*, 1990). In a minor modification of the published procedure, polyvinylpyrrolidone (100 mg/g tissue) was added prior to addition of CTAB isolation buffer. The DNA was digested with either *EcoRI* or *EcoRI* and *HindIII*. *EcoRI* cleaves the region between the borders of the binary vector once, and therefore produces

junction fragments. The *EcoRI* and *HindIII* double digest produces a single intra-border 4.7kb *SAMase* fragment.

Complete digestion of the DNA was confirmed using a hybridization probe for the strawberry alcohol dehydrogenase gene, *ADH* (Wolyn, et al., 1990). The probe was also used as a relative measure of the DNA content in each lane.

EXAMPLE 9

ROOTING AND TRANSPLANTATION OF TRANSGENIC STRAWBERRY

Individual shoots (about 20-30 mm in length) isolated from multiple shoot clumps cultured on proliferation medium were cultured on rooting medium containing half strength MS (Murashige and Skoog, 1962) salts, B5 (Gamborg et al., 1968) vitamins, 1% sucrose, 100 mg/l carbenicillin, with selection agent.

The choice of selection agent was dependent upon the plasmid used in transformation. For shoots transformed with the plasmids, pAG5110, pAG5520 and pAG1552, 60 mg/l kanamycin or 15 mg/l geneticin was used. Shoots transformed with the plasmid, pAG1452, were cultured on rooting medium containing 10 mg/l hygromycin.

Inhibition experiments carried out on control non-transformed shoots revealed that kanamycin, at levels of 25 mg/l, and hygromycin, at levels of less than 5 mg/l, completely inhibited root formation.

Following storage in the greenhouse for about 2-4 days, well-rooted plants were rinsed to remove adherent media and potted in soil.

EXAMPLE 10

TRANSGENIC STRAWBERRY: CULTIVAR TRISTAR

Meristematic segments of cv. Tristar were transformed with the binary vector pAG5110 in either of the disarmed strains of *A. tumefaciens*, LBA4404 or EHA101, and cultured on regeneration medium containing either 0, 10 or 25 mg/l kanamycin. In about 3 weeks, formation of shoot initials from the meristematic segments was observed in each of the three treatments. Explants from all three treatments were transferred to medium containing 50 mg/l kanamycin, followed by subsequent transfer to medium containing 75 mg/l kanamycin.

During periods of subculture, completely bleached tissues were discarded while fully or partially green tissues were maintained. Fully or partially green shoots were longitudinally segmented while transferring to fresh medium.

After 4 months of culture, the percent recovery of putative strawberry transformants consistently able to proliferate in the presence of selection agent exhibited a direct correlation to the level of selection in the initial screening medium. Exposure to zero level of selection during the first 3 weeks resulted in recovery of no or few putative transformants. Explants transformed with the binary vector pAG5110 in disarmed *A. tumefaciens* strain LBA4404 exhibited transformation frequencies for shoot regeneration of 0.0%, 2.3%, 13.6% for culture treatments in which the media contained 0, 10 and 25 mg/l kanamycin, respectively. Explants transformed with the binary vector pAG5110 in disarmed *A. tumefaciens* strain EHA101 exhibited transformation frequencies for shoot regeneration of 2.5%, 11.6% and 16.7%, corresponding to increasing levels of kanamycin, as described above.

Histochemical analysis of regenerants on selection medium showed a mixture of completely blue shoots and shoots with some blue regions (Figs. 6,7).

EXAMPLE 11

20

TRANSGENIC STRAWBERRY: CULTIVAR TOTEM

A. TRANSFORMATION AND PLANT REGENERATION.

Cultivar Totem was transformed with binary vectors containing DNA sequences encoding the SAMase gene and the selectable marker genes *nptII* or *hpt* (for resistance to kanamycin and hygromycin, respectively) in the disarmed *A. tumefaciens* strains EHA101 or EHA105, as described in Example 7.

After co-cultivation, explants of cultivar Totem were cultured on regeneration medium containing either 50 mg/l kanamycin or 10 mg/l hygromycin, depending upon the plasmid used for transformation. After 3 weeks, bleached or necrotic tissues were discarded (Fig. 8). Explants with callus and/or shoot regenerants were segmented longitudinally and transferred to medium containing either 75 mg/l kanamycin or 15 mg/l hygromycin.

Initial explant identity was maintained for different segments. At the higher levels of selection agent, some segments were completely bleached or necrosed, while other segments were capable of withstanding the increased level of selection

and produced shoot regenerants. Individual shoot regenerants were isolated and cultured on shoot proliferation medium containing 100-150 mg/l kanamycin or 40-50 mg/l hygromycin.

5 Petiole, leaf and shoot base explants were isolated from shoots exhibiting proliferation in the presence of increased levels of selection agent. The petiole, leaf and shoot base explants were recultured on regeneration medium containing 150 mg/l kanamycin or 40 mg/l hygromycin (Fig. 9).

10 If any of the segments of an event underwent bleaching or necrosis, the source regenerant was determined to be a chimera. Iterative culture was then continued until no part of the shoot regenerants showed sensitivity to selection (Fig. 13). Subsequent to screening to remove chimeric transformants, the regenerated shoots were multiplied on proliferation medium containing 200 mg/l kanamycin or 70 mg/l hygromycin, depending on the plasmid constructs.

15 A summary of the transformation frequencies from different experiments in cultivar Totem is provided in Table 2. In experiments ST10 through ST14 (Table 2), equal numbers of explants were screened on regeneration medium containing silver nitrate. In contrast to green compact callus and profuse shoot regenerants on silver nitrate-free screening medium, the explants on medium supplemented with silver nitrate produced friable yellow callus with occasional regenerants.

20 Ninety five to 100% of the transgenic shoots successfully rooted on medium containing 60 mg/l kanamycin or 10 mg/l hygromycin (Figs. 5 and 10, Table 2). Well-rooted transgenic plants were quickly established in soil with nearly 100 percent success (Fig. 11). The total duration of time from explant co-cultivation with *A.tumefaciens* to transfer of transgenics to soil was about 8-10 months.

TABLE 2

FREQUENCY OF TRANSFORMATION IN
STRAWBERRY, CULTIVAR TOTEM

| Exper. ID | Agro Strain/ Binary Vector | Selection | Explant, # | Trans. Freq. % | Trans. Events Recvr'd | Events Rooted |
|--|-------------------------------|------------|-------------------------------|----------------|-----------------------|---------------|
| ST10-1A | EHA101/- pAG5520 | Kanamycin | leaf 31 | 35.5 | 11 | 11 |
| | | | mer. seg. 149 | 46.9 | 70 | 68 |
| ST11-1A | EHA105/- pAG5520 | Kanamycin | leaf 17 | 58.8 | 10 | 9 |
| | | | mer. seg. 147 | 40.8 | 60 | 59 |
| ST12-1 | EHA101/- pAG5520 | Kanamycin | leaf 40 | 32.5 | 13 | 13 |
| ST13-1 | EHA105/- pAG4420 | Kanamycin | leaf 40 | 12.5 | 5 | 4 |
| ST14-1 | EHA101/- pAG5520 | Kanamycin | young shoot segments 195 | 33.3 | 65 | 65 |
| ST20 | EHA105/- pAG1452 | Hygromycin | young shoot segments 122 2 | 15.6 | 191 | 182 |
| 1. Trans. freq. = transformation frequency, see "Results" for definition. 2. Trans. events = Transformation events, see "Results" for definition. 3. Mer. seg. = Meristematic segment. | | | | | | |

B. SOUTHERN HYBRIDIZATION

Southern blot data (Figs. 12A-C) showed a variety of transgene copy numbers and integration structures. The DNA from transgenic plant leaves (plasmid pAG5520) was digested with either *EcoRI* alone or in conjunction with *HindIII*, as described in Example 8. The *EcoRI* digest allows determination of the number of individual integration events while the double digest allows an estimation of the total transgene copy number for that event.

As seen in Fig. 12C, the last panel represents the *EcoRI* blot containing a hybridization probe for the strawberry alcohol dehydrogenase gene. The *EcoRI* blot indicates single integration events for lanes 4 and 6 and multiple events in lanes 5 and 7. The combined *EcoRI* and *HindIII* blot (Fig. 12B) confirms the multiple gene copy number for lanes 5 and 7 and indicates that an aberrant integration occurred in the event shown in lane 5 due to a smaller than expected fragment hybridizing to the SAMase probe. The signal strength in lanes 4 and 6 is identical to that of the *EcoRI* blot (Fig. 12A), confirming the single integration status for these two events. The differences in hybridization signal strength is not attributable to a difference in DNA amounts, since the *EcoRI* blot probed with the strawberry ADH gene showed similar signal intensities for lanes 4 through 7. The identical band pattern seen with the ADH probe clearly indicates complete digestion, validating the interpretation of multiple events for lanes 5 and 7.

A single integration event for strawberry (an octoploid) is expected to be eight-fold lower than for a native gene such as ADH. A comparison of the band intensities in lanes 4 and 6 for the SAMase-probed blots (Figs. 12A,B) and the ADH probed blot (Fig. 12C) reveals a corresponding difference of approximately eight-fold.

20

EXAMPLE 12

IMPACT OF ANTIBIOTICS ON STRAWBERRY TRANSFORMANTS

In a separate experiment to examine the effects different antibiotics on the selection of transformants, leaf and petiole explants from cultivar Totem (transformed with the plasmid pAG1552) were co-cultivated with *A.tumefaciens* strain EHA105. The transformed explants were screened on medium supplemented with either kanamycin or geneticin.

The explants cultured on medium containing geneticin either became brown or produced scanty callus with poor rates of shoot regeneration (Table 3).

Transgenic shoots (confirmed by Southern hybridization), consistently prolific on medium containing kanamycin, were similarly cultured on geneticin-containing medium. The resulting explants, cultured in the presence of geneticin, exhibited a tendency for browning and declining proliferation with increasing passages.

Clonal transgenic shoots, capable of profuse rooting in the presence of 60 mg/l kanamycin, did not root on medium containing 15 mg/l geneticin.

TABLE 3**EFFECT OF KANAMYCIN VS. GENETICIN ON RECOVERY
OF TRANSFORMANTS IN CV. TOTEM**

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| Exper. ID | Agro strain/binary vector | Selection | Explant, # | Trans. Freq. % | Trans. Events Recvr'd |
|-----------|---------------------------|-----------|-------------|----------------|-----------------------|
| ST21-1 | EHA105/pAG1552 | Kanamycin | leaf 329 | 15.5 | 51 |
| | | Kanamycin | petiole 131 | 16.0 | 21 |
| ST21-2 | EHA105/pAG1552 | Geneticin | leaf 293 | 1.3 | 4 |
| | | Geneticin | petiole 132 | 2.3 | 3 |

1. Trans. freq. = Transformation frequency, see "Results" for definition.

2. Trans. events = Transformation events, see "Results" for definition.

20

Taken together, these results suggest kanamycin is a superior selection agent when compared to geneticin for both shoot regeneration and rooting.

While the invention has been described with reference to specific methods and embodiments, it will be appreciated that various modifications and changes may be made without departing from the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Epitope, Inc.
- (C) CITY: Beaverton
- (D) STATE: OR
- (E) COUNTRY: USA
- (F) POSTAL CODE: 97005

(ii) TITLE OF INVENTION: Plant Genetic Transformation
Methods and Transgenic Plants

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Dehlinger & Associates
- (B) STREET: 350 Cambridge Avenue, Suite 250
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94306

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/384,556
- (B) FILING DATE: 03-FEB-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/263,900
- (B) FILING DATE: 17-JUN-1994

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Fabian, Gary R.
- (B) REGISTRATION NUMBER: 33,875

(C) REFERENCE/DOCKET NUMBER: 4257-0010.41

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 324-0880

(B) TELEFAX: (415) 324-0960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: SAM-K

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 66..521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACAGCTATGA CCATGATTAC GCCAAGCTTG CATGCCTGCA GGTCGACTCT AGAGGATCCG 60

CCACC ATG GTT TTC ACT AAA GAG CCT GCG AAC GTC TTC TAT GTA CTG 107

Met Val Phe Thr Lys Glu Pro Ala Asn Val Phe Tyr Val Leu

1 5 10

GTT TCC GCT TTC CGT TCT AAC CTC TGC GAT GAG GTG AAT ATG AGC AGA 155

Val Ser Ala Phe Arg Ser Asn Leu Cys Asp Glu Val Asn Met Ser Arg

15 20 25 30

CAC CGC CAC ATG GTA AGC ACT TTA CGT GCC GCA CCG GGT CTT TAT GGC 203

His Arg His Met Val Ser Thr Leu Arg Ala Ala Pro Gly Leu Tyr Gly

35 40 45

TCC GTT GAG TCA ACC GAT TTG ACC GGG TGC TAT CGT GAG GCA ATC TCA 251

Ser Val Glu Ser Thr Asp Leu Thr Gly Cys Tyr Arg Glu Ala Ile Ser

43

| | | | |
|---|-----|-----|-----|
| 50 | 55 | 60 | |
| AGC GCA CCA ACT GAG GAA AAA ACT GTT CGT GTA CGC TAC AAG GAC AAA | | | 299 |
| Ser Ala Pro Thr Glu Glu Lys Thr Val Arg Val Arg Tyr Lys Asp Lys | | | |
| 65 | 70 | 75 | |
| GCG CAG GCA CTC AAT GTT GCA CGC CTA GCT TGT AAT GAG TGG GAG CAA | | | 347 |
| Ala Gln Ala Leu Asn Val Ala Arg Leu Ala Cys Asn Glu Trp Glu Gln | | | |
| 80 | 85 | 90 | |
| GAT TGC GTA CTG GTA TAC AAA TCA CAG ACT CAC ACG GCT GGT CTG GTG | | | 395 |
| Asp Cys Val Leu Val Tyr Lys Ser Gln Thr His Thr Ala Gly Leu Val | | | |
| 95 | 100 | 105 | 110 |
| TAC GCT AAA GGT ATC GAC GGG TAT AAG GCT GAA CGT CTG CCG GGT AGT | | | 443 |
| Tyr Ala Lys Gly Ile Asp Gly Tyr Lys Ala Glu Arg Leu Pro Gly Ser | | | |
| 115 | 120 | 125 | |
| TTC CAA GAG GTT CCT AAA GGC GCA CCG CTG CAA GGC TGC TTC ACT ATT | | | 491 |
| Phe Gln Glu Val Pro Lys Gly Ala Pro Leu Gln Gly Cys Phe Thr Ile | | | |
| 130 | 135 | 140 | |
| GAT GAG TTC GGT CGC CGC TGG CAA GTA CAA TAAGTGTTAA ACTCAAGGTC | | | 541 |
| Asp Glu Phe Gly Arg Arg Trp Gln Val Gln | | | |
| 145 | 150 | | |
| ATGCACGATG CGTGGCGGAT CCGGTACCGA GCTCGAATTC ACTGG | | | 586 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | |
|---|----|----|----|
| Met Val Phe Thr Lys Glu Pro Ala Asn Val Phe Tyr Val Leu Val Ser | | | |
| 1 | 5 | 10 | 15 |
| Ala Ph Arg Ser Asn Leu Cys Asp Glu Val Asn Met Ser Arg His Arg | | | |
| 20 | 25 | 30 | |

44

His Met Val Ser Thr Leu Arg Ala Ala Pro Gly Leu Tyr Gly Ser Val
 35 40 45

Glu Ser Thr Asp Leu Thr Gly Cys Tyr Arg Glu Ala Ile Ser Ser Ala
 50 55 60

Pro Thr Glu Glu Lys Thr Val Arg Val Arg Tyr Lys Asp Lys Ala Gln
 65 70 75 80

Ala Leu Asn Val Ala Arg Leu Ala Cys Asn Glu Trp Glu Gln Asp Cys
 85 90 95

Val Leu Val Tyr Lys Ser Gln Thr His Thr Ala Gly Leu Val Tyr Ala
 100 105 110

Lys Gly Ile Asp Gly Tyr Lys Ala Glu Arg Leu Pro Gly Ser Phe Gln
 115 120 125

Glu Val Pro Lys Gly Ala Pro Leu Gln Gly Cys Phe Thr Ile Asp Glu
 130 135 140

Phe Gly Arg Arg Trp Gln Val Gln
 145 150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Tomato E8 promoter region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCATTT TTGACATCCC TAATGATATT GTTCACGTAA TTAAGTTTGG TGGAAGTGAG

60

| | |
|--|------|
| AGAGTCCAAT TTTGATAAGA AAAGAGTCAG AAAACGTAAT ATTTTAAAAG TCTAAATCTT | 120 |
| TCTACAAATA AGAGCAAATT TATTTATTTT TTAATCCAAT AAATATTAAT GGAGGACAAA | 180 |
| TTCAATTCAC TTGGTTGTAA AATAAACTTA AACCAATAAC CAAAGANCTA ATAAATCTGA | 240 |
| AGTGGAATTA TTAAGGATAA TGTACATAGA CAATGAAGAA ATAATAGGTT CGATGAATTA | 300 |
| ATAATAATTA AGGATGTTAC AATCATCATG TGCCAAGTAT ATACACAATA TTCTATGGGA | 360 |
| TTTATAATTT CGTTACTTCA CTTAACTTTT GCGTAAATAA AACGAATTAT CTGATATTTT | 420 |
| ATAATAAAAC AGTTAATTAA GAACCATCAT TTTTAACAAC ATAGATATAT TATTTCTAAT | 480 |
| AGTTTAATGA TACTTTTAAA TCTTTTAAAT TTTATGTTTC TTTTAGAAAA TAAAAATTCA | 540 |
| AAAAAATTAA ATATATTTAC AAAAACTACA ATCAAACACA ACTTCATATA TTAAAAGCAA | 600 |
| AATATATTTT GAAAATTCA AGTGTCTTAA CAAATAAGAC AAGAGGAAAA TGTACGATGA | 660 |
| GAGACATAAA GAGAACTAAT AATTGAGGAG TCCTATAATA TATAATAAAG TTTATTAGTA | 720 |
| AACTTAATTA TTAAGGACTC CTAAATATA TGATAGGAGA AAATGAATGG TGAGAGATAT | 780 |
| TGGAAAACCTT AATAATTAAG GATNTTAAAA TATATGGTAA AAGATAGGCA AAGTATCCAT | 840 |
| TATCCCCTTT TAACTTGAAG TCTACCTAGG CGCATGTGAA AGGTTGATT TTTGTCACGT | 900 |
| CATATAGCTA TAACGTAAAA AAAGAAAGTA AAATTTTAA TTTTTTTTAA TATATGACAT | 960 |
| ATTTTAAACG AAATATAGGA CAAAATGTAA ATGAATAGTA AAGGAAACAA AGATTAATAC | 1020 |
| TTACTTTGTA AGAATTTAAG ATAAATTTAA AATTTAATAG ATCAACTTTA CGTCTAGAAA | 1080 |
| GACCCATATC TAGAAGGAAT TTCACGAAAT CGGCCCTTAT TCAAAAATAA CTTTTAAATA | 1140 |
| ATGAATTTTA AATTTTAAGA AATAATATCC AATGAATAAA TGACATGTAG CATTTTACCT | 1200 |
| AAATATTTCA ACTATTTTAA TCCAATATTA ATTTGTTTTA TTCCCAACAA TAGAAAGTCT | 1260 |
| TGTGCAGACA TTTAATCTGA CTTTTCAGT ACTAAATATT AATTTTCTGA AGATTTTCGG | 1320 |
| GTTTAGTCCA CAAGTTTTAG TGAGAAGTTT TGCTCAAAAT TTTAGGTGAG AAGGTTTGAT | 1380 |
| ATTTATCTTT TGTTAAATTA ATTTATCTAG GTGACTATTA TTTATTTAAG TAGAAATTCA | 1440 |

| | |
|---|------|
| TATCATTACT TTTGCCAACT TGTAGTCATA ATAGGAGTAG GTGTATATGA TGAAGGAATA | 1500 |
| AACAAGTTCA GTGAAGTGAT TAAAATAAAA TATAATTTAG GTGTACATCA AATAAAAACC | 1560 |
| TTAAAGTTTA GAAAGGCACC GAATAATTTT GCATAGAAGA TATTAGTAAA TTTATAAAAA | 1620 |
| TAAAAGAAAT GTAGTTGTCA AGTTGTCTTC TTTTTTTTGG ATAAAATAG CAGTTGGCTT | 1680 |
| ATGTCATTCT TTTACAACCT CCATGCCACT TGTCCAATTG TTGACACTTA ACTAATTAGT | 1740 |
| TTGATTCATG TATGAATACT AAATAATTTT TTAGGACTGA CTCAAATATT TTTATATTAT | 1800 |
| CATAGTAATA TTTATCTAAT TTTTAGGACC ACTTATTACT AAATAATAAA TTAACACTA | 1860 |
| CTATATTATT GTTGTGAAAC AACAACGTTT TGGTTGTTAT GATGAAACGT ACACTATATC | 1920 |
| AGTATGAAAA ATTCAAACG ATTAGTATAA ATTATATTGA AAATTGATA TTTTCTATT | 1980 |
| CTTAATCAGA CGTATTGGGT TTCATATTTT AAAAAGGGAC TAAACTTAGA AGAGAAGTTT | 2040 |
| GTTTGAAACT ACTTTTGTCT CTTTCTTGTT CCCATTTCTC TCTTAGATTT CAAAAAGTGA | 2100 |
| ACTACTTTAT CTCTTCTTT GTTCACATTT TATTTTATTC TATTATAAAT ATGGCATCCT | 2160 |
| CATATTGAGA TTTTLAGAAA TTATTCTAAT CATTACAGT GCAAAGACC ATGGAA | 2216 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: E4 tomato gene DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1439..1774

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1439..1774

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1859..2113

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1859..2113

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 1775..1858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|---|-----|
| GAATTCTCAA TTGAGCCCAA TTCAATCTCC AATTTCAACC CGTTTTAAAA CTTTTTATTA | 60 |
| AGATATGTTT CTATATTGAA AGTATGAATT ATTATCTATT TAACATCTTT TAGGATTTAT | 120 |
| CTATCCATTT GCTACTTTTT TAACAAAAAA TTCTTGAGTG AAAATTCAAA TTGTGATTAT | 180 |
| AAAAGTTAAA TATCAATATG TTAAATTATT AAGATTAATC GGGTCAAATT GGCGGGTCAA | 240 |
| GGCCCAATTC TTTTITAGCC CATTTAAGCT CAAAGTAAAC TTGGGTGGGT CAAGACCCAA | 300 |
| CTCGATTCT GTTCAACCCA TTTTAATATT TCTATTTTCA ACCTAACCCG CTCATTTGAT | 360 |
| ACCCCTACAA ATATCATATT TGTGTGTGAA ATATTTTTTG GGCTGGAGAG AGAGGCCCCG | 420 |
| AGGGGAGTGG AGGGGTGGGG TGGGGAGAGA GAGCGAGAAA GAGTGGAGAG AGAAATTTGA | 480 |
| TATGAAATCC TACATATATT ACAGATTGTA ATGTTCTAAA CTATAACGAT TTGTCATAAA | 540 |
| CACATATCAT GGATTTGTCT TTTTGTGTAA TTTTCCAAT TGTAATAGG ACTTCGTTAT | 600 |
| TTGAACTTG AAAGTGAAGT CACATAGATT AAGTACAAAC ATTAATTAAA GACCGTGGTG | 660 |
| GAATGATAAA TATTTATTTA TCTTTAATTA GTTATTTTTT TGGGAGCTCT TTATTCCAAT | 720 |
| GTGAGACTTT TGCGACATAT ATTCAAATTT AATCGAATCA CAATATGTAT TAGATTGATA | 780 |

| | |
|---|------|
| AAAAATAAT TTTTACAA TGTTAGTTGA GACTCATAAC TTACTGCCTA TTGGTAATCT | 840 |
| ATGACTCCTA ATTCCTTAAT TATTAAATA TATCATCTTG ATCGTTAACA AAGTAATTC | 900 |
| GAAAGACCAC GAGTAAGAAG ACAACGAGA ATACCAAAA ATTCAAAAT TTAATGTGAT | 960 |
| TTGGTCAATC GATCTACGTC CATAAAGGAG ATGAGTAATC TACTATAAAT ATGAGAGTAC | 1020 |
| AAAATACAGA GAGAAACAAC CTCAACTAAT TCACTCGGAA TACATGAGAA GTTCACACAA | 1080 |
| GTGATAACGT ATCAAACCTG TGACCCACAC TTTCCCTCT AACCAAAGCT CTTAAACTA | 1140 |
| TATTGTGAAT GCTGATTAAG TTAAACGAAA CAGTCCTAAA TCTTTCCGT CCTATGAGAA | 1200 |
| ACAAGATTAA TCAATTCACA ATTTTAAATA AAAGAAAAC CTGTAAGAAA TTTAGGCAA | 1260 |
| CAAAACCTAA CACAAGTTTG TTTTGTGTTT TACTACCAAC AAGAAATCA AATGGCAAAT | 1320 |
| GTATAACGCA TCTTAGCTAA TTATATGACC AGATTCAGAT TAATATACAT CTTACCCAT | 1380 |
| GCAATCCATT TCTATATAAA GAAACATACA CGAACTTGAT ATTATTAGAG ATTGAGCA | 1438 |
| ATG GAG GGT AAC AAC AGC AGT AGC AAG TCA ACC ACC AAT CCA GCA TTG | 1486 |
| Met Glu Gly Asn Asn Ser Ser Ser Lys Ser Thr Thr Asn Pro Ala Leu | |
| 1 5 10 15 | |
| GAT CCG GAT CTG GAC AGC CCG GAT CAG CCG GGT CTG GAG TTT GCC CAA | 1534 |
| Asp Pro Asp Leu Asp Ser Pro Asp Gln Pro Gly Leu Glu Phe Ala Gln | |
| 20 25 30 | |
| TTT GCT GCC GGC TGC TTT TGG GGA GTC GAA TTG GCT TTC CAG AGG GTT | 1582 |
| Phe Ala Ala Gly Cys Phe Trp Gly Val Glu Leu Ala Phe Gln Arg Val | |
| 35 40 45 | |
| GGA GGA GTA GTG AAG ACG GAG GTT GGG TAC TCT CAG GGG AAT GTC CAT | 1630 |
| Gly Gly Val Val Lys Thr Glu Val Gly Tyr Ser Gln Gly Asn Val His | |
| 50 55 60 | |
| GAC CCG AAC TAC AAG CTT ATT TGC TCC GGA ACA ACC GAA CAT GCC GAG | 1678 |
| Asp Pro Asn Tyr Lys Leu Ile Cys Ser Gly Thr Thr Glu His Ala Glu | |
| 65 70 75 80 | |
| GCC ATT CGG ATC CAG TTT GAC CCG AAT GTC TGC CCG TAT TCC AAT CTC | 1726 |
| Ala Ile Arg Ile Gln Phe Asp Pro Asn Val Cys Pro Tyr Ser Asn Leu | |
| 85 90 95 | |

| | |
|---|------|
| CTT TCT CTA TTT TGG AGT CGC CAT GAC CCG ACC ACT CTA AAT CGC CAG | 1774 |
| Leu Ser Leu Phe Trp Ser Arg His Asp Pro Thr Thr Leu Asn Arg Gln | |
| 100 105 110 | |
| GTATCAAATT CCTTTGGTGT TTCATTTTAT GTGATTAATA TAAAAAATTT TTTATATAAA | 1834 |
| TGTCATGATG ATGGTTGTTG CTAG GGT AAT GAT GTG GGA AAG CAA TAC CGC | 1885 |
| Gly Asn Asp Val Gly Lys Gln Tyr Arg | |
| 1 5 | |
| TCA GGA ATA TAT TAC TAT AAT GAT GCT CAG GCT CAA CTG GCA AGG GAG | 1933 |
| Ser Gly Ile Tyr Tyr Tyr Asn Asp Ala Gln Ala Gln Leu Ala Arg Glu | |
| 10 15 20 25 | |
| TCG TTA GAA GCT AAG CAG AAG GAA TTT ATG GAT AAG AAA ATT GTC ACT | 1981 |
| Ser Leu Glu Ala Lys Gln Lys Glu Phe Met Asp Lys Lys Ile Val Thr | |
| 30 35 40 | |
| GAA ATT CTT CCT GCT AAG AGA TTT TAT AGA GCT GAA GAG TAT CAC CAG | 2029 |
| Glu Ile Leu Pro Ala Lys Arg Phe Tyr Arg Ala Glu Glu Tyr His Gln | |
| 45 50 55 | |
| CAA TAT CTA GAG AAG GGT GGG GGC AGA GGT TGT AAG CAG TCG GCT GCA | 2077 |
| Gln Tyr Leu Glu Lys Gly Gly Gly Arg Gly Cys Lys Gln Ser Ala Ala | |
| 60 65 70 | |
| AAG GGC TGC AAT GAC CCA ATA AGG TGC TAC GGT TGACAGCAGA TCTTTGAATG | 2130 |
| Lys Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly | |
| 75 80 85 | |
| TCATAGCAAC TACAAAAGAA CTTGTTAGAC ATTTGCTGTC TTGCTTCTTT AAATTTGAAT | 2190 |
| AAACATGACA ATGATTCTTA TAACTACTTG CTCTCTTGA TGAATAACT AGTTGTCGTA | 2250 |
| AAGTATTCTC CTCTTGCTAA TTATTATCTC TCTTTATATG GTACCTGCAA TTTGTTGCTT | 2310 |
| TAGTTACAGA ATAATGGACG TCAATTCTAT ATCTTAATTT GTTTTAAGTC TTAAATGAGG | 2370 |
| TGTTTGTGT TTGAAAGCAA TATCAAGCAT AGTAATACCA ATGATTTAGT AGATGAACTT | 2430 |
| AATCAAATCA AATTCCAAAA TGCAGTCTAC AAATTGACAA CATGAAGTTA AGTGATCTT | 2490 |
| ATGTAAATTG ACATCTTTCC TAGTAGATGC CTAATACTTT TGTAAGACT AAAATAAGCA | 2550 |
| CAGATGAGGC TTGTGCATTT AACTTAGAGT TCATCCTTAG GTGTGGCTGC AGGAGACCCT | 2610 |

GTAGGGTTGC TTGAAGTCTT GATGGGGTAG GAGGGTTGCA TTGCTATACC ACACAACCCC 2670
 TCTTCAGCGT CAACCTTGCG CTGCATTCTA ATGTATCCTT TTTCTCCCCA TTCAGCTCCC 2730
 CATGAGTTCT TCACAATCCA GTATTGGTT CCATCGACGG TTGTGCCATA CCCCACAATA 2790
 GCCACA 2796

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Gly Asn Asn Ser Ser Ser Lys Ser Thr Thr Asn Pro Ala Leu
 1 5 10 15
 Asp Pro Asp Leu Asp Ser Pro Asp Gln Pro Gly Leu Glu Phe Ala Gln
 20 25 30
 Phe Ala Ala Gly Cys Phe Trp Gly Val Glu Leu Ala Phe Gln Arg Val
 35 40 45
 Gly Gly Val Val Lys Thr Glu Val Gly Tyr Ser Gln Gly Asn Val His
 50 55 60
 Asp Pro Asn Tyr Lys Leu Ile Cys Ser Gly Thr Thr Glu His Ala Glu
 65 70 75 80
 Ala Ile Arg Ile Gln Phe Asp Pro Asn Val Cys Pro Tyr Ser Asn Leu
 85 90 95
 Leu Ser Leu Phe Trp Ser Arg His Asp Pro Thr Thr Leu Asn Arg Gln
 100 105 110
 Gly Asn Asp Val Gly Lys Gln Tyr Arg Ser Gly Ile Tyr Tyr Tyr Asn
 115 120 125
 Asp Ala Gln Ala Gln Leu Ala Arg Glu Ser Leu Glu Ala Lys Gln Lys
 130 135 140

51

Glu Phe Met Asp Lys Lys Ile Val Thr Glu Ile Leu Pro Ala Lys Arg
 145 150 155 160

Phe Tyr Arg Ala Glu Glu Tyr His Gln Gln Tyr Leu Glu Lys Gly Gly
 165 170 175

Gly Arg Gly Cys Lys Gln Ser Ala Ala Lys Gly Cys Asn Asp Pro Ile
 180 185 190

Arg Cys Tyr Gly
 195

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: E4 tomato promoter /
 AdoMetase gene DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1174..1629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCTTAAAG TAAACTTGGG TGGGTCAAGA CCCAACTCGA TTTCTGTTCA ACCCATTTTA 60
 ATATTTCTAT TTTCAACCTA ACCCGTCAT TTGATACCCC TACAAATATC ATATTTGTGT 120
 GTGAAATATT TTTTGGGCTG GAGAGAGAGG CCCCAGGGG AGTGGAGGGG TGGGGTGGGG 180
 AGAGAGAGCG AGAAGAGTG GAGAGAGAAA TTTGATATGA AATCCTACAT ATATTACAGA 240
 TTGTAATGTT CTAACTATA ACGATTTGTC ATAAACACAT ATCATGGATT TGTCTTTTGT 300

| | |
|---|------|
| TGTAATTTTC CCAATTGTAA ATAGGACTTC GTTATTTGAA ACTTGAAAGT GAAGTCACAT | 360 |
| AGATTAGTA CAAACATTAA TTAAAGACCG TGGTGAATG ATAAATATTT ATTTATCTTT | 420 |
| AATTAGTTAT TTTTTTGGGA GCTCTTTATT CCAATGTGAG ACTTTTGCGA CATATATTCA | 480 |
| AATTTAATCG AATCACAATA TGTATTAGAT TGATAAAAAA ATAATTTTTT TACAATGTTA | 540 |
| GTTGAGACTC ATAACCTACT GCCTATTGGT AATCTATGAC TCCTAATTCC TTAATTATTT | 600 |
| AAATATATCA TCTTGATCGT TAACAAAGTA ATTTGAAAG ACCACGAGTA AGAAGACAAA | 660 |
| CGAGAATACC AAAAAATTCA AAAATTTAAT GTGATTTGGT CAATCGATCT ACGTCCATAA | 720 |
| AGGAGATGAG TAATCTACTA TAAATATGAG AGTACAAAAT ACAGAGAGAA ACAACCTCAA | 780 |
| CTAATTCACT CGGAATACAT GAGAAGTTCA CACAAGTGAT AACGTATCAA ACTTGTGACC | 840 |
| CACACTTTTC CCTCTAACCA AAGCTCTTAA AACTATATTG TGAATGCTGA TTAAGTTAAA | 900 |
| CGAAACAGTC CTAAATCTTT TCCGTCCTAT GAGAAACAAG ATTAATCAAT TCACAATTTT | 960 |
| TTTAAAAAGA AAAACCTGTA AGAAATTTAG GCAAACAAAA CCTAACACAA GTTTGTTTTT | 1020 |
| GTTTTTACTA CCAACAAGAA ATTCAAATGG CAAATGTATA ACGCATCTTA GCTAATTATA | 1080 |
| TGACCAGATT CAGATTAATA TACATCTTCA CCCATGCAAT CCATTTCTAT ATAAAGAAAC | 1140 |
| ATACACGAAC TTGATATTAT TAGAGATTGA GCC ATG GTT TTC ACT AAA GAG CCT | 1194 |
| Met Val Phe Thr Lys Glu Pro | |
| 1 5 | |
| GCG AAC GTC TTC TAT GTA CTG GTT TCC GCT TTC CGT TCT AAC CTC TGC | 1242 |
| Ala Asn Val Phe Tyr Val Leu Val Ser Ala Phe Arg Ser Asn Leu Cys | |
| 10 15 20 | |
| GAT GAG GTG AAT ATG AGC AGA CAC CGC CAC ATG GTA AGC ACT TTA CGT | 1290 |
| Asp Glu Val Asn Met Ser Arg His Arg His Met Val Ser Thr Leu Arg | |
| 25 30 35 | |
| GCC GCA CCG GGT CTT TAT GGC TCC GTT GAG TCA ACC GAT TTG ACC GGG | 1338 |
| Ala Ala Pro Gly Leu Tyr Gly Ser Val Glu Ser Thr Asp Leu Thr Gly | |
| 40 45 50 55 | |
| TGC TAT CGT GAG GCA ATC TCA AGC GCA CCA ACT GAG GAA AAA ACT GTT | 1386 |

53

| | |
|---|------|
| Cys Tyr Arg Glu Ala Ile Ser Ser Ala Pro Thr Glu Glu Lys Thr Val | |
| 60 65 70 | |
| CGT GTA CGC TAC AAG GAC AAA GCG CAG CCA CTC AAT GTT GCA CGC CTA | 1434 |
| Arg Val Arg Tyr Lys Asp Lys Ala Gln Pro Leu Asn Val Ala Arg Leu | |
| 75 80 85 | |
| GCT TCT AAT GAG TGG GAG CAA GAT TGC GTA CTG GTA TAC AAA TCA CAG | 1482 |
| Ala Ser Asn Glu Trp Glu Gln Asp Cys Val Leu Val Tyr Lys Ser Gln | |
| 90 95 100 | |
| ACT CAC ACG GCT GGT CTG GTG TAC GCT AAA GGT ATC GAC GGG TAT AAG | 1530 |
| Thr His Thr Ala Gly Leu Val Tyr Ala Lys Gly Ile Asp Gly Tyr Lys | |
| 105 110 115 | |
| GCT GAA CGT CTG CCG GGT AGT TTC CAA GAG GTT CCT AAA GGC GCA CCG | 1578 |
| Ala Glu Arg Leu Pro Gly Ser Phe Gln Glu Val Pro Lys Gly Ala Pro | |
| 120 125 130 135 | |
| CTG CAA GGC TGC TTC ACT ATT GAT GAG TTC GGT CGC CGC TGG CAA GTA | 1626 |
| Leu Gln Gly Cys Phe Thr Ile Asp Glu Phe Gly Arg Arg Trp Gln Val | |
| 140 145 150 | |
| CAA TAACGTGTTA AACTCAAGGT CATGCACGAT GCGTGGCGGA TCGGGTACC | 1678 |
| Gln | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| |
|---|
| Met Val Phe Thr Lys Glu Pro Ala Asn Val Phe Tyr Val Leu Val Ser |
| 1 5 10 15 |
| Ala Phe Arg Ser Asn Leu Cys Asp Glu Val Asn Met Ser Arg His Arg |
| 20 25 30 |
| His Met Val Ser Thr Leu Arg Ala Ala Pro Gly Leu Tyr Gly Ser Val |

54

| | | |
|---|-----|-----|
| 35 | 40 | 45 |
| Glu Ser Thr Asp Leu Thr Gly Cys Tyr Arg Glu Ala Ile Ser Ser Ala | | |
| 50 | 55 | 60 |
| Pro Thr Glu Glu Lys Thr Val Arg Val Arg Tyr Lys Asp Lys Ala Gln | | |
| 65 | 70 | 75 |
| Pro Leu Asn Val Ala Arg Leu Ala Ser Asn Glu Trp Glu Gln Asp Cys | | |
| | 85 | 90 |
| Val Leu Val Tyr Lys Ser Gln Thr His Thr Ala Gly Leu Val Tyr Ala | | |
| 100 | 105 | 110 |
| Lys Gly Ile Asp Gly Tyr Lys Ala Glu Arg Leu Pro Gly Ser Phe Gln | | |
| 115 | 120 | 125 |
| Glu Val Pro Lys Gly Ala Pro Leu Gln Gly Cys Phe Thr Ile Asp Glu | | |
| 130 | 135 | 140 |
| Phe Gly Arg Arg Trp Gln Val Gln | | |
| 145 | 150 | |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: raspberry E4 gene DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55

GAG CTC AGG TTT CAG CGA GTG GCC GGT GTG GTC AAG ACC GAG GTT GGG 48
 Glu Leu Arg Phe Gln Arg Val Ala Gly Val Val Lys Thr Glu Val Gly
 1 5 10 15

TAC TCC CAG GGC CAC GTC CAC GAT CCG AAT TAC AAA CTG GTC TGC TCC 96
 Tyr Ser Gln Gly His Val His Asp Pro Asn Tyr Lys Leu Val Cys Ser
 20 25 30

GGA ACT ACC AAC CAT TCG GAG GTC GTT CGG GTC CAG TTC GAC CCG CAA 144
 Gly Thr Thr Asn His Ser Glu Val Val Arg Val Gln Phe Asp Pro Gln
 35 40 45

GTC TAC CCA TAC TCG GAC CTG CTT TCC GTC TTT TGG TCT CGT CAT GAT 192
 Val Tyr Pro Tyr Ser Asp Leu Leu Ser Val Phe Trp Ser Arg His Asp
 50 55 60

CCA ACG ACT GTC AAT CGC CAG GTATGGGGAT TG 225
 Pro Thr Thr Val Asn Arg Gln
 65 70

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Leu Arg Phe Gln Arg Val Ala Gly Val Val Lys Thr Glu Val Gly
 1 5 10 15

Tyr Ser Gln Gly His Val His Asp Pro Asn Tyr Lys Leu Val Cys Ser
 20 25 30

Gly Thr Thr Asn His Ser Glu Val Val Arg Val Gln Phe Asp Pro Gln
 35 40 45

Val Tyr Pro Tyr Ser Asp Leu Leu Ser Val Phe Trp Ser Arg His Asp
 50 55 60

Pro Thr Thr Val Asn Arg Gln
 65 70

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: RASPBERRY E4 GENE

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1468..1469
- (D) OTHER INFORMATION: /note= "small sequencing gap of unknown size"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|---|-----|
| AAGCTTAATT GAGATGATTA GCCCAGACCC AGCAGGATTA GGCTTAATGG TGGTCCATT | 60 |
| GAGAAAAAGA TTAAAAATGA TGTCAATAAA AACNTGGTC GBCAGGATTC NAACCTGCCG | 120 |
| GGGCAAAGCC ACATGATTTC TAGTCATGCC CGATAACCAC TCCGGCACGA CCACAATGAT | 180 |
| GCTACAATTG CTTTGTTGTA ATCATTAACT TATGGTTGAG TTTGATGCTG ATTAATACTA | 240 |
| TTATGTTTCC ATTAACACT TTTGAAGTAT ACAAATTAC GAATTTATAA CCAAATTTGA | 300 |
| GGTATAATAT GCGAGAGCTA CCTAAATTTT TCTTACTTAA TTTTAAAGTA CATTCAAATT | 360 |
| CTGAATTTAT ATTGTGTATA GTCAGAAAAC AATCTACATA TTTAAACACA TAAATTTCTC | 420 |
| ACGTTTATAA TCAATTTTGT CGGTTCTCTG AATTTTCTA AAATAAAAAG CAACCAAAT | 480 |
| TGTGCATCAA CTTATTACAT ACCATGGGAA ATGCAACTT CAAACTTAT GGA CTCAAAG | 540 |
| GGTACATATC TAACTACAT ATTGTCAGAT TCTTCACTCT TATTTCTTGA GGGCCTCGAG | 600 |

| | |
|--|------|
| GCATTACCAA CCAAATCCAA AAATTGCTTT CGAATCTCAA TAAAAAGGAT AACCCCATGA | 660 |
| AAAAGACGTG GACGGCAGGA TTCGAACCTG CGCGCAGAGC CCACATGATT TCTAGTCATG | 720 |
| CCCGATAACC ACTCOGGCAC GTCCACTTCA CTGTTAACGT TTACAGTAAC AAGTCACTAA | 780 |
| CTACTAATCA ACATTAGCTC AGGAAATCAA AACTAGATTA TTTACATTTA CAACGACATG | 840 |
| TCGTTCGAAG TAGTTGGTCT GTATCTGAGT AGCTTTGGCG GGTAGATTCA ATCGCATTTT | 900 |
| TGCATATAAA ACTGATCCTC CCTCTATCGC CAAAGTCAA CTGAAAATGG CTTCCACCAC | 960 |
| CACCAACAAC CCAGCTCTAG ACCCAGATTC GGACACTCCG GATAATCCGG GTCACGAGTT | 1020 |
| TGCTCAATTC GGATCCGGGT GCTTCTGGGG AGCCGAGCTC AGGTTTCAGC GAGTGGCCCG | 1080 |
| TGTGGTCAAG ACCGAGGTTG GGTACTCCCA GGGCCACGTC CACGATCCGA ATTACAACT | 1140 |
| GGTCTGCTCC GGAACACCA ACCATTCGGA GGTGTTCCG GTCCAGTTCG ACCCGCAAGT | 1200 |
| CTACCCATAC TCGGACCTGC TTTCCGTCTT TTGGTCTCGT CATGATCCAA CGACTGTCAA | 1260 |
| TCGCCAGGTA TGGGGATTGG GGACTTCTGT TTTTATTGTA ATTTTGATGC TAAAAATTT | 1320 |
| CTTGCTTTTT CATACTACAC AGTACACACA AAAAGTTGTG TTTTTTTTCA TTCTTTTAAA | 1380 |
| TAGTAGTTGG AAAAGTGCTC TTGGAGTTGA AGAGTACTTC AGTATTGCAT ATGGTCTCAG | 1440 |
| TGAAATGATA GTGATTATCA TAAGGAGTTT AAAGGCAGGA TGCATTTTGT GTATGANTGA | 1500 |
| TTTTGGGTAG AATATTTTTG GAACAGTTAA AATTTATGGG CTGCTGCACA CTGGCTATGA | 1560 |
| ACAAATGTAT AGCATTAAAG TGCTTATGAC AAATTCACAA TTGTATATTA GCAGCAGAGA | 1620 |
| CATTAAAGTT TCTAAATGCC TTTTAAGTAG ATTGGAAAAA AGTGCTTTTT TTGGTTGAAG | 1680 |
| AAGCACATTC ACTATTTGCC TGTTAATGGA ATTGGTAATG ATGAATCACA AGGATATTTG | 1740 |
| TGAATACAAG CAGGATGCTT TTAGTGTGCA AGTGATCTTT CGGAACATTT AAAATCGTCA | 1800 |
| TAACAAAGGT GTAACATAAG AAGGCTTTGA AATATTCTCA ATTTCTCATT GATTGAATGA | 1860 |
| ATTATGTGTT AGGGTGGAGA TGTGGGTACT CAATATCGAT CTGGAATATA CTACTIONAAC | 1920 |
| GAAACGCAGG CCCGTCTAGC ACAGGAATCA AAGGAAGCAA AGCAACTCGA GTTTAAGGAT | 1980 |

| | |
|---|------|
| AAGAAGGTGG TGACAGAGAT TCTTCCAGCA AAGAGGTTTT ACAGGGCAGA GGAGTACCAT | 2040 |
| CAGCAATATC TCGCAAAGGG AGGAGGTAAT GGCAACAAAC AATCTGCTGA AAAAGGTTGC | 2100 |
| AATGATCCTA TTCGATGCTA TGGTTGAGAA ACTAATGCAT TATGCCATTA TTAAACTCT | 2160 |
| ACTGGTTTAC TATGCAGAAA CACCTATGTC AGTTCAATTA TACTGAAGGC ACCAAAGTGT | 2220 |
| CATCTTAAAT TATATGGCAA TGTTTTACTC GTTATGAATA AAGGAGGTCC AAGTCGACCA | 2280 |
| GATATGAACA AATGAAATAT TGCCATGTTA ATTGGAATCC AGTAGTAATT AGGATTTGTT | 2340 |
| TTGGTGTATG TACTCCGATA TCAAGATATG CAAATGATGC ATTGTGTTTT TATATATTGA | 2400 |
| CAAGTTCCAA ATTATAGTAC TTCGTATGTG TTATGCGGTT TAATTAGTGT TGCTTACTTG | 2460 |
| AATGGTATAT TACTATTATG CTTAGTAGGA ACTAGGAACT AGGGAATATG TTGTGATAGA | 2520 |
| GTTGTCCAAC GAAATTTTGT ACCAAAGTTA TTTCATTGAA TAAAACTAC AGTCTTAGAG | 2580 |
| ATACATCCAA TTCTATAAAG TGAAAGAAGC AAATATTATT TGTTCATGAG GCTATGAGTC | 2640 |
| ATGAACTTTA TGCTATAACC GAAGCAACCT CAGAAAAGTC GAAGTAAATT GTGTATTGTT | 2700 |
| TAGAGCTC | 2708 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: RASPBERRY E4 PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

59

Met Ala Ser Thr Thr Thr Asn Asn Pro Ala Leu Asp Pro Asp Ser Asp
 1 5 10 15

Thr Pro Asp Asn Pro Gly His Glu Phe Ala Gln Phe Gly Ser Gly Cys
 20 25 30

Phe Trp Gly Ala Glu Leu Arg Phe Gln Arg Val Ala Gly Val Val Lys
 35 40 45

Thr Glu Val Gly Tyr Ser Gln Gly His Val His Asp Pro Asn Tyr Lys
 50 55 60

Leu Val Cys Ser Gly Thr Thr Asn His Ser Glu Val Val Arg Val Gln
 65 70 75 80

Phe Asp Pro Gln Val Tyr Pro Tyr Ser Asp Leu Leu Ser Val Phe Trp
 85 90 95

Ser Arg His Asp Pro Thr Thr Val Asn Arg Gln Gly Gly Asp Val Gly
 100 105 110

Thr Gln Tyr Arg Ser Gly Ile Tyr Tyr Tyr Asn Glu Thr Gln Ala Arg
 115 120 125

Leu Ala Gln Glu Ser Lys Glu Ala Lys Gln Leu Glu Phe Lys Asp Lys
 130 135 140

Lys Val Val Thr Glu Ile Leu Pro Ala Lys Arg Phe Tyr Arg Ala Glu
 145 150 155 160

Glu Tyr His Gln Gln Tyr Leu Ala Lys Gly Gly Gly Asn Gly Asn Lys
 165 170 175

Gln Ser Ala Glu Lys Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly
 180 185 190

IT IS CLAIMED:

1. A method for producing transgenic plants, comprising:
 - (i) introducing a vector into cells of a target explant under conditions to generate transformation of explant cells by said vector,
5 where said vector has a first DNA sequence that encodes a gene encoding a selectable marker functional in plant cells, where said first DNA sequence is flanked by regulatory elements effective to allow expression of the sequence in plant host cells, and where expression of said gene produces a gene product that confers the ability of plant cells expressing the gene to grow in the presence of a selective agent,
 - 10 (ii) screening said transformed explant cells by culturing transformed explants in selective media having a threshold concentration of selective agent,
 (iii) culturing the explants under regeneration conditions to produce regenerated shoots,
 (iv) generating explants from the regenerated shoots,
 - 15 (v) culturing the transformed explants on a higher concentration of selective agent,
 (vi) repeating steps (ii) through (v) until pure transgenic explants are obtained, and
 (vii) producing transgenic plants by regenerating plants from the pure transgenic explants.
- 20 2. A method of claim 1, where said vector is an *Agrobacterium* vector.
3. A method of claim 2, where said introducing includes cultivating a target explant in the presence of *Agrobacterium* containing the vector under conditions to generate transformation of explant cells by said vector.
25
4. A method of claim 3, where said cultivating is carried out in liquid culture.
5. A method of claim 4, where said cultivating is carried out for 1 to 3 days.
- 30 6. A method of claim 1, where said explant is an explant selected from the group consisting of leaf, meristem and petiole.

7. A method of claim 1, where said pure transgenic explants are identified by dividing the regenerated shoots into explants, culturing the explants, and verifying that the growth of all explants is resistant to the highest concentration of selective agent used.

5 8. A method of claim 1, where said selective agent is selected from the group consisting of hygromycin, geneticin, and kanamycin.

9. A method of claim 1, where said gene encoding a selectable marker functional in plant cells is *NPTII* or *hpt*.

10

10. A method of claim 1, where the vector further includes a second DNA sequence which is flanked by regulatory elements effective to allow expression of the sequence in plant cells.

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11. A method of claim 10, where said second DNA sequence encodes a product that is effective to reduce ethylene biosynthesis in fruit from the plant or increase the sugar content in fruit from the plant.

20

12. A method of claim 10, wherein said DNA sequence encodes S-adenosyl-methionine hydrolase.

25

13. A method of claim 10, wherein said DNA sequence encodes a product selected from the group consisting of aminocyclopropane-1-carboxylic acid (ACC) deaminase, ACC oxidase antisense molecule, ACC synthase antisense molecule, ACC oxidase cosuppression molecule, and ACC synthase cosuppression molecule.

14. A method of claim 10, where said second DNA sequence encodes a product that is effective to increase plant and/or fruit fungal resistance or viral resistance.

30

15. A method of claim 10, where said regulatory elements flanking the second DNA sequence include a tissue or stage specific promoter.

16. A method of claim 1, wherein the transformation of explant cells is carried out by a direct transformation methodology selected from the group consisting of electroporation, microinjection, and microprojectile bombardment.
- 5 17. A method of claim 1, wherein the plant produces a fruit, vegetable or flower.
18. A method of claim 1, where said plant is a red raspberry plant.
19. A method of claim 1, where said plant is a strawberry plant.
- 10 20. A pure transgenic plant of any of claims 1 through 19.
21. A pure transgenic plant tissue explant of any of claims 1 through 19.
- 15 22. A pure transgenic fruit produced by a transgenic plant of any of claims 1 through 19.
23. A pure transgenic vegetable or flower produced by a transgenic plant of any of claims 1 through 17.
- 20 24. A transgenic plant cell from a transgenic plant of any of claims 1 through 19.
25. A seed produced by a transgenic plant of any of claims 1 through 19.
- 25 26. A pure transgenic regenerated plant shoot of any of claims 1 through 19.
27. A pure transgenic strawberry plant.
28. A transgenic strawberry of claim 27, where said plant encodes a DNA
30 sequence that encodes a product that is effective to reduce ethylene biosynthesis in fruit from the plant or increase the sugar content in fruit from the plant.
29. A transgenic strawberry plant of claim 28, wherein said DNA sequence encodes S-adenosylmethionine hydrolase.

30. A transgenic strawberry plant of claim 28, wherein said DNA sequence encodes a product selected from the group consisting of aminocyclopropane-1-carboxylic acid (ACC) deaminase, ACC oxidase antisense molecule, ACC synthase antisense molecule, ACC oxidase cosuppression molecule, and ACC synthase cosuppression molecule.

5

31. A transgenic strawberry of claim 27, where said plant encodes a DNA sequence that encodes a product that is effective to increase plant and/or fruit fungal resistance or viral resistance.

10

32. A pure transgenic strawberry fruit.

33. A pure transgenic strawberry fruit produced by a transgenic plant of any of claims 27 through 31.

15

34. A pure transgenic red raspberry plant.

35. A transgenic red raspberry plant of claim 34, where said plant encodes a DNA sequence that encodes a product that is effective to reduce ethylene biosynthesis in fruit from the plant or increase the sugar content in fruit from the plant.

20

36. A transgenic red raspberry plant of claim 35, wherein said DNA sequence encodes S-adenosylmethionine hydrolase.

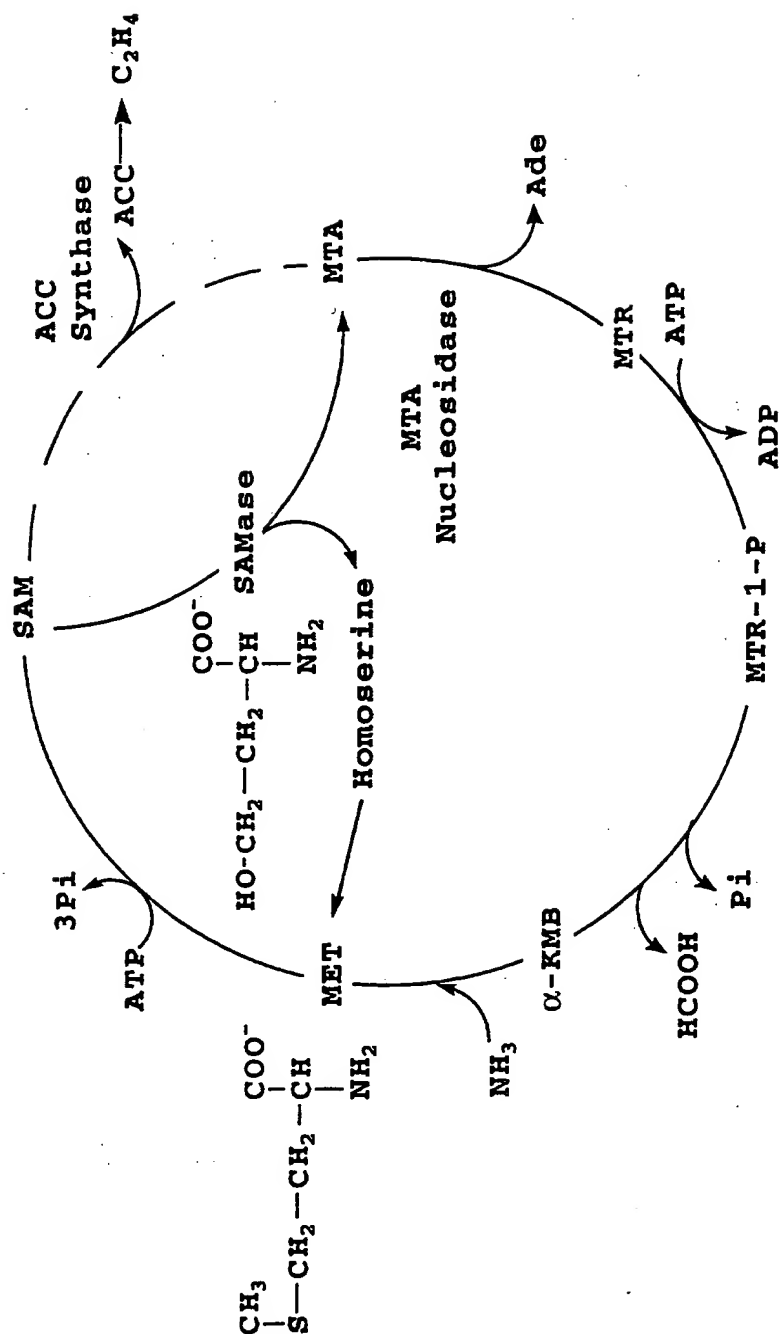
37. A transgenic red raspberry plant of claim 35, wherein said DNA sequence encodes a product selected from the group consisting of aminocyclopropane-1-carboxylic acid (ACC) deaminase, ACC oxidase antisense molecule, ACC synthase antisense molecule, ACC oxidase cosuppression molecule, and ACC synthase cosuppression molecule.

38. A transgenic red raspberry plant of claim 34, where said plant encodes a DNA sequence that encodes a product that is effective to increase plant and/or fruit fungal resistance or viral resistance.

39. A pure transgenic red raspberry fruit.

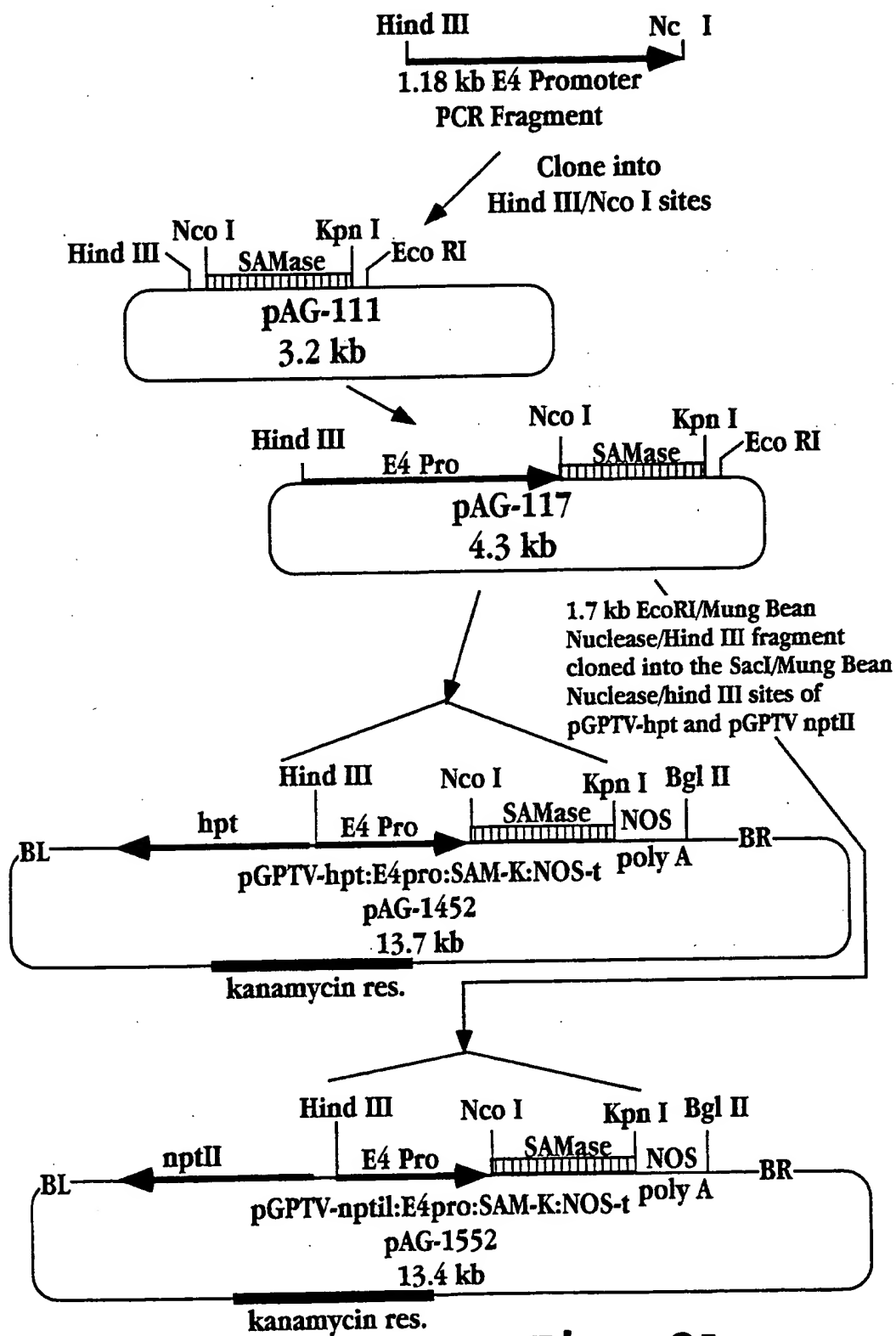
40. A pure transgenic red raspberry fruit produced by a transgenic plant of any of claims 34 through 38.

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16.5.

2/14

**Fig. 2A**

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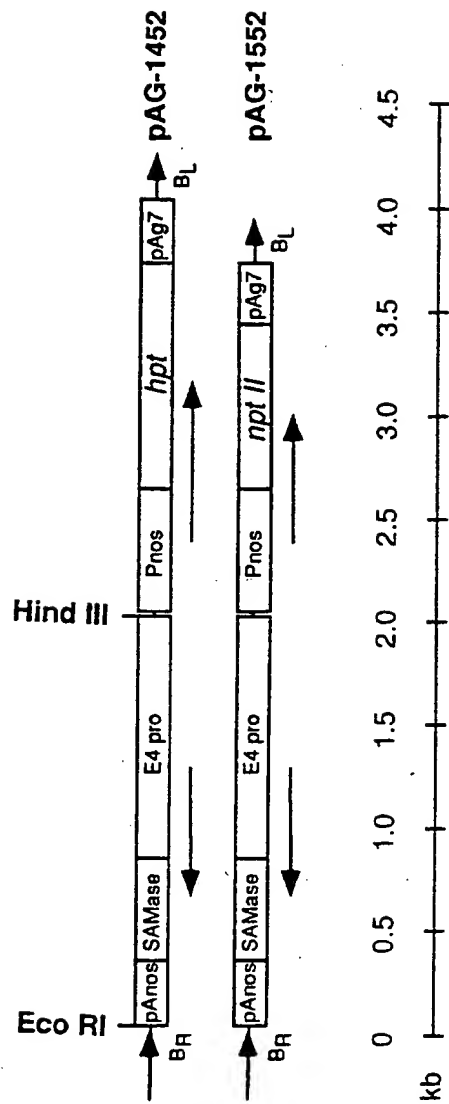


Fig. 2B

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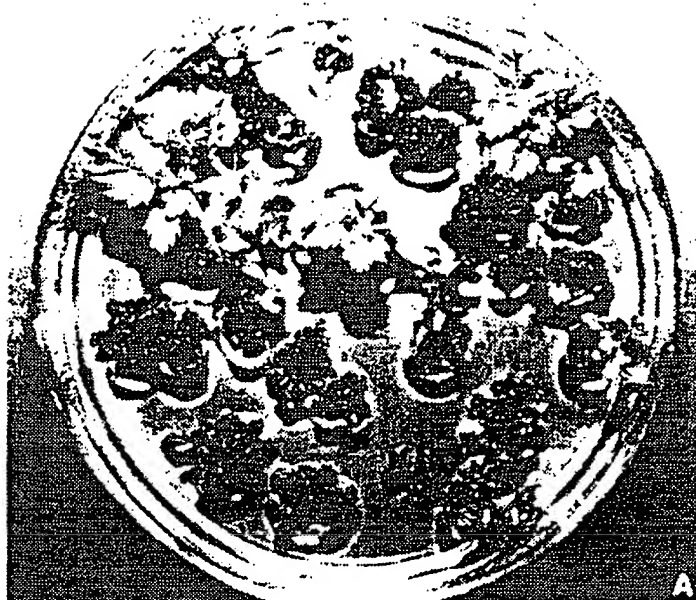


Fig. 3A

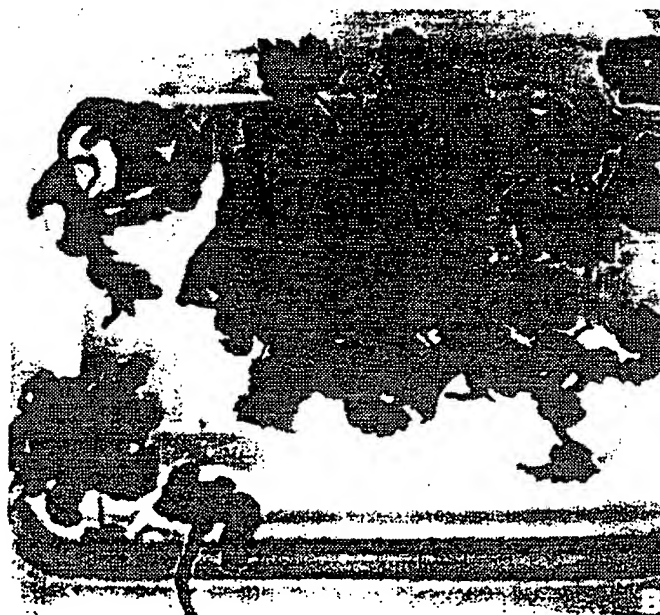


Fig. 3B

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Fig. 3C



Fig. 3D

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Fig. 3E

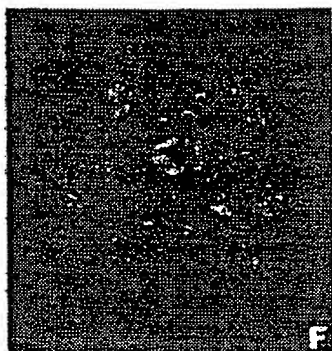
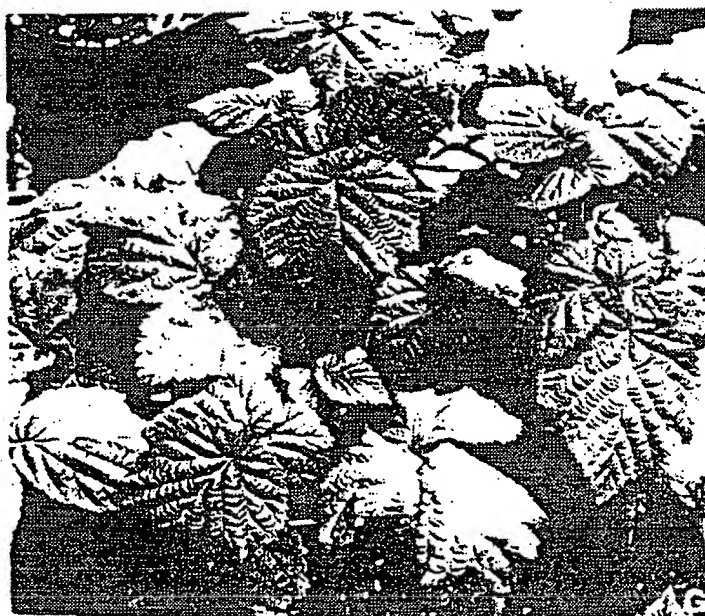


Fig. 3F

Fig. 3G



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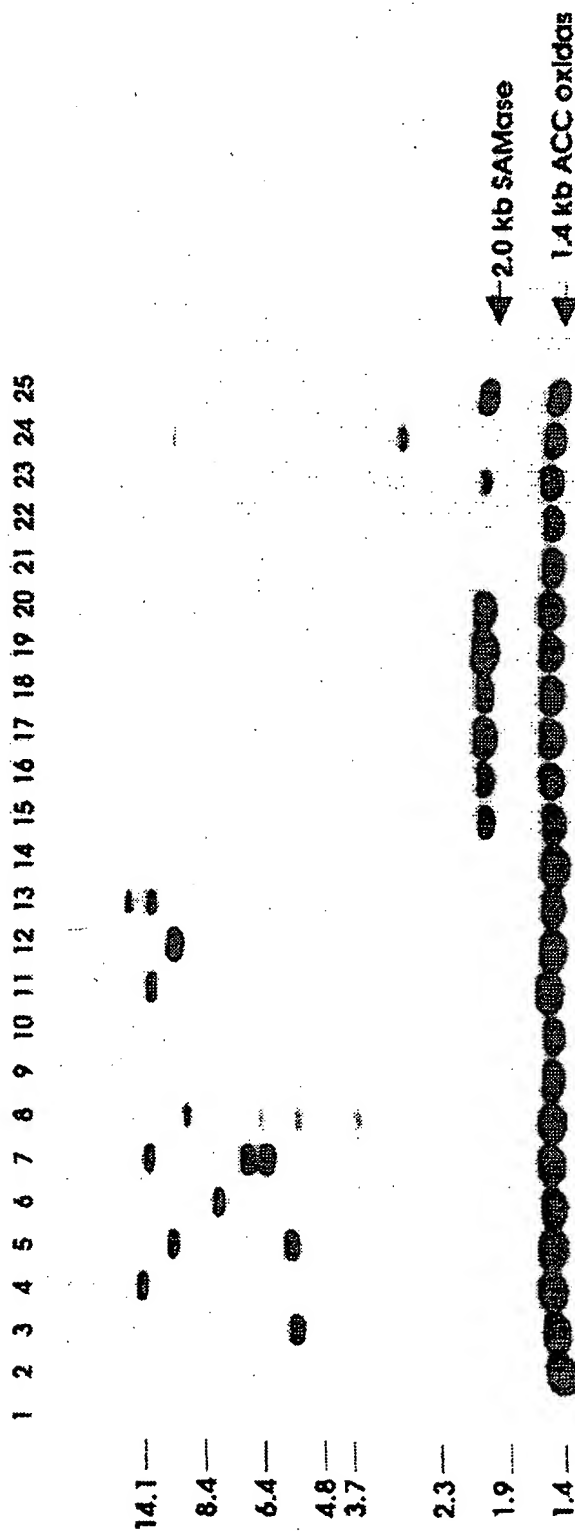


Fig. 4A

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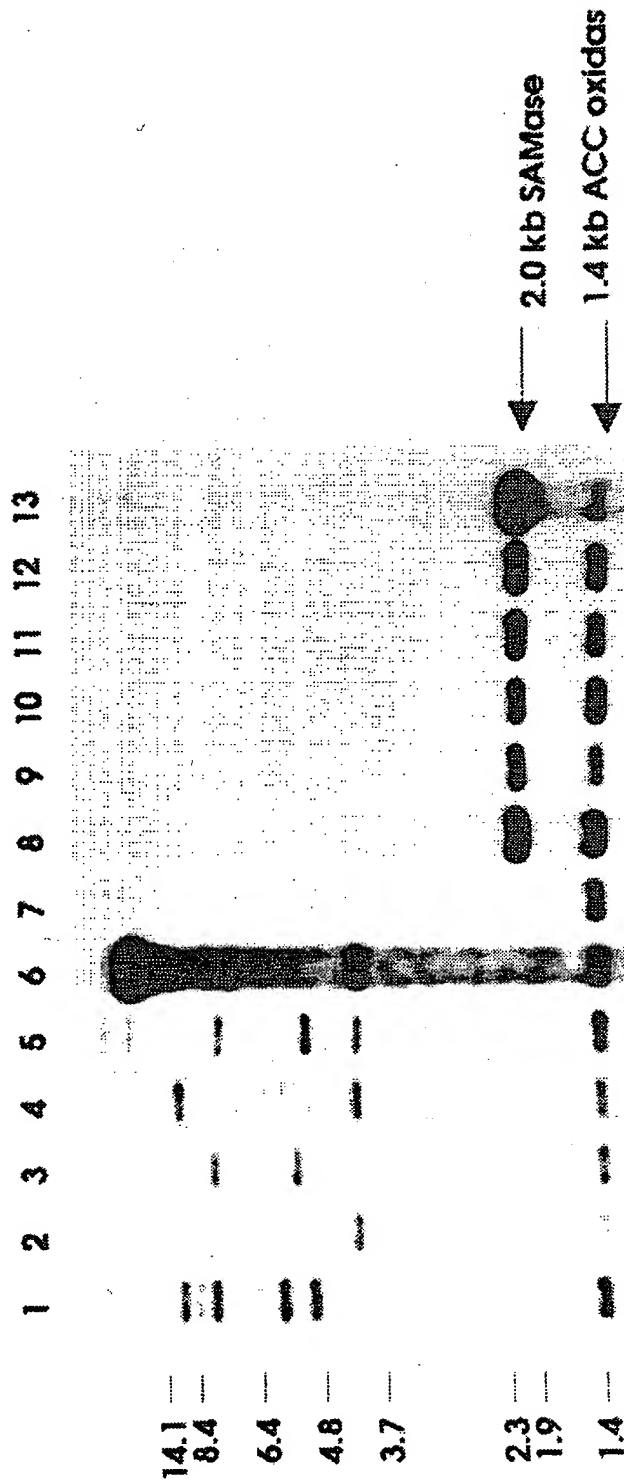


Fig. 4B

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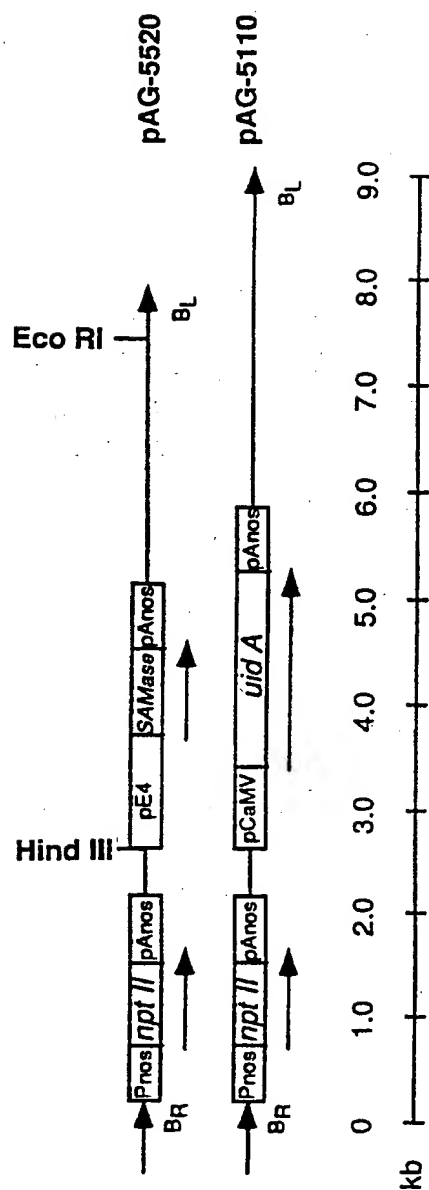


Fig. 5

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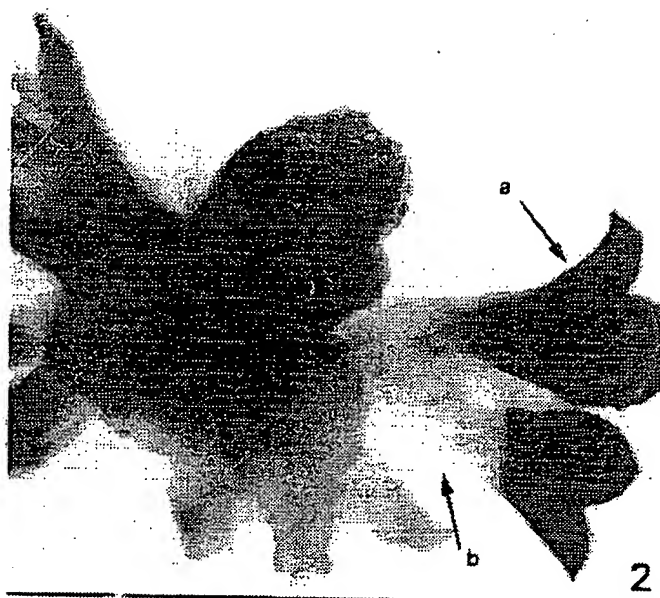


Fig. 6



Fig. 7

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Fig. 8



Fig. 9

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Fig. 10



Fig. 11

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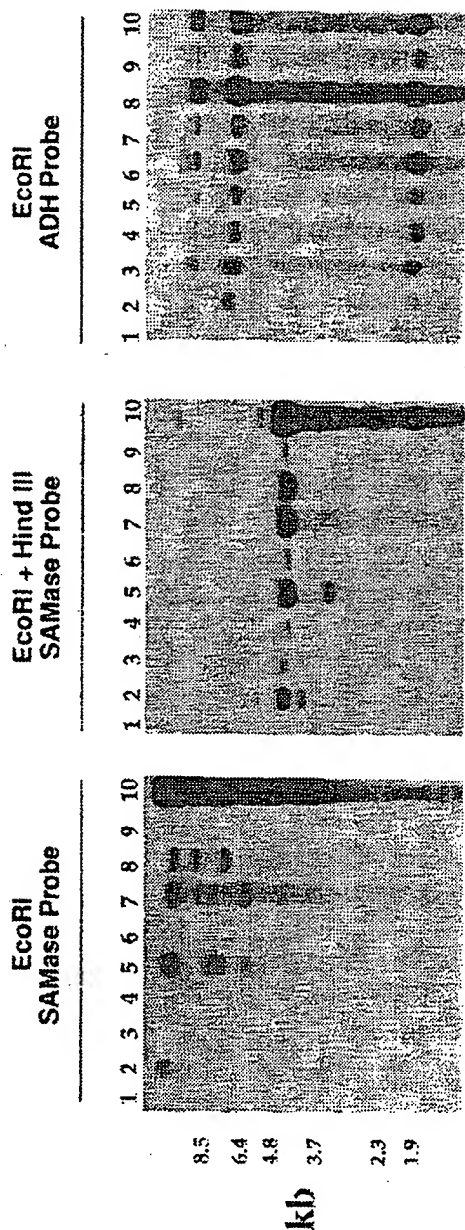


Fig. 12A Fig. 12B Fig. 12C

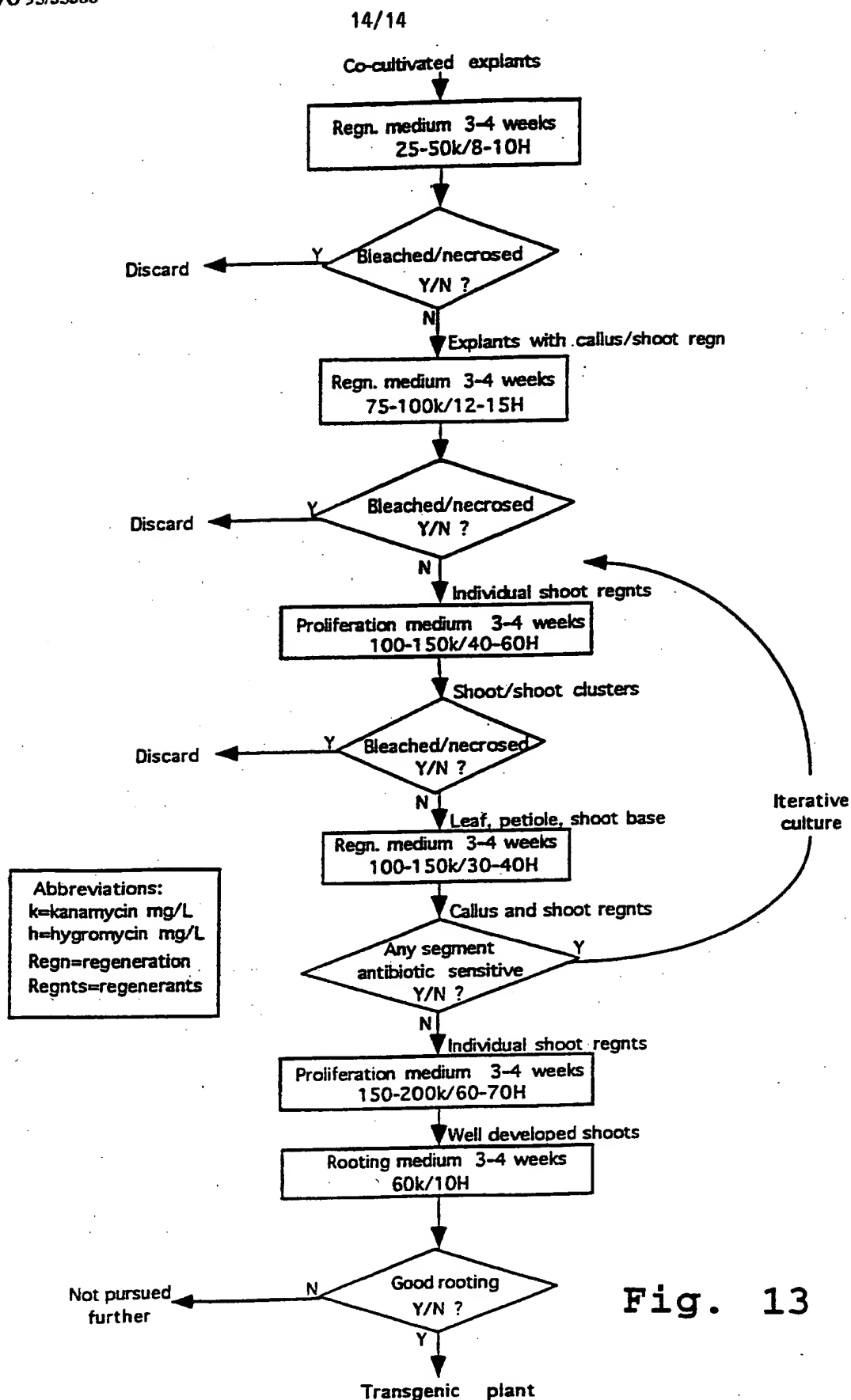


Fig. 13

INTERNATIONAL SEARCH REPORT

Internat'l Application No

PCT/US 95/07753

| A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/82 C12N15/60 C12N15/55 C12N15/53 A01H5/00 | | |
|---|---|--|
| According to International Patent Classification (IPC) or to both national classification and IPC | | |
| B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N A01H | | |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched | | |
| Electronic data base consulted during the international search (name of data base and, where practical, search terms used) | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X | HORTSCIENCE, vol. 29, no. 5, May 1994 page 454 MATHEWS, H., ET AL. 'GENETIC TRANSFORMATION OF RED RASPBERRY (RUBUS IDAEUS L.) WITH A GENE TO CONTROL ETHYLENE BIOSYNTHESIS' | 1-12, 15, 17, 18, 20-22, 24-26, 34-36, 39, 40 |
| Y | see abstract 180 | 13, 16, 19, 37 |
| Y | WO,A,92 12249 (MONSANTO CO) 23 July 1992 see page 25, line 1 - line 8 | 13, 28, 30, 33, 37 |
| Y | US,A,5 240 839 (SERRES) 31 August 1993 see the whole document | 16 |
| -/-- | | |
| <input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex. | | |
| * Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "A" document member of the same patent family | | |
| Date of the actual completion of the international search 23 October 1995 | | Date of mailing of the international search report 22. 11. 95 |
| Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016 | | Authorized officer Maddox, A |

INTERNATIONAL SEARCH REPORT

International Application No

PCT/us 95/07753

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|----------|--|-----------------------|
| Y | PLANT CELL REPORTS, vol. 11, 1992 pages 105-108, NYMAN, M., ET AL. 'TRANSIENT GENE EXPRESSION IN STRAWBERRY (FRAGARIA X ANANASSA DUCH.) PROTOPLASTS AND RECOVERY OF TRANSGENIC PLANTS' see the whole document ---- | 16 |
| X | PLANT CELL REPORTS, vol. 9, no. 6, 1990 pages 293-298, NEHRA, N.S., ET AL. 'GENETIC TRANSFORMATION OF STRAWBERRY BY AGROBACTERIUM-TUMEFACIENS USING A LEAF DISK REGENERATION SYSTEM' see the whole document ---- | 27,32,33 |
| Y | WO,A,91 09112 (AGRITOP INC) 27 June 1991 see page 14, line 8 - line 10 ---- | 19, 28-30,33 |
| Y | WO,A,91 09112 (AGRITOP INC) 27 June 1991 see page 14, line 8 - line 10 ---- | 28,29,33 |
| X | PLANT SCIENCE, vol. 69, no. 1, 1990 pages 79-94, JAMES, D.J., ET AL. 'AGROBACTERIUM-MEDIATED TRANSFORMATION OF THE CULTIVATED STRAWBERRY FRAGARIA-ANANASSA DUCH. USING DISARMED BINARY VECTORS' see the whole document ---- | 27,32,33 |
| Y | PLANT CELL REPORTS, vol. 9, 1990 pages 10-13, NEHRA, N.S., ET AL. 'AGROBACTERIUM-MEDIATED TRANSFORMATION OF STRAWBERRY CALLI AND RECOVERY OF TRANSGENIC PLANTS' see the whole document ---- | 28-30,33 |
| X | PLANT CELL REPORTS, vol. 9, 1990 pages 10-13, NEHRA, N.S., ET AL. 'AGROBACTERIUM-MEDIATED TRANSFORMATION OF STRAWBERRY CALLI AND RECOVERY OF TRANSGENIC PLANTS' see the whole document ---- | 27,32,33 |
| X | PLANT CELL TISSUE ORGAN CULTURE, vol. 33, no. 1, 1993 pages 9-17, HASSAN, M.A., ET AL. 'AGROBACTERIUM-TUMEFACIENS MEDIATED TRANSFORMATION OF SEVERAL RUBUS GENOTYPES AND RECOVERY OF TRANSFORMED PLANTS' see the whole document ---- | 34,39,40 |

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 95/07753

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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